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Best Local Similarity 92.2%; Pred. No. 3.8e-145;
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LOCUS Sequence 1 from Patent WO0155219.
DEFINITION
ACCESSION AX205042
VERSION AX205042.1 GI:15394277
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Elson, G. and Gauchat, J.F.
TITLE Scentifer/ant-1 fusion protein
JOURNAL Patent: WO 0155219-A 1 02-AUG-2001;
PIERRE FABRE MEDICAMENT (FR)
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HLGANGP"
BASE COUNT 158 a 318 c 246 g 159 t
ORIGIN
Query Match 82.3%; Score 674; DB 6; Length 881;
Best Local Similarity 92.2%; Pred. No. 3.8e-145;
Matches 721; Conservative 0; Mismatches 60; Indels 1; Gaps 1;
2 ATTATTAAGCTTCCCGGAGCCGCGGCTCCGCTCCCACTCCGACGCTCTGGAGAG 61
82 ATTATTAAGCTTCCCGGAGCCGCGGCTCCGCTCCCACTCCGACGCTCTGGAGAG 141
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RESULT 3 AF176913 819 bp mRNA linear ROD 04-OCT-1999
 LOCUS AF176913
 DEFINITION Mus musculus neurotrophin-1/B-cell stimulating factor-3 mRNA,
 complete cds.
 ACCESSION AF176913
 VERSION AF176913.1 GI:6007644
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 819)
 Sensi, G., Varnum, B.C., Sarmiento, U., Starnes, C., Lile, J.,
 Scully, S., Guo, J., Elliott, G., McNinch, J., Shaklee, C.E.,
 Freeman, D., Mann, F., Simone, W.S., Boone, T. and Chang, M.S.
 Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
 IL-6 family
 TITLE Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)
 JOURNAL 99432254
 MEDLINE 10500198
 PUBMED

REFERENCE 2 (bases 1 to 819)
 Sensi, G., Varnum, B., Sarmiento, U., Lile, J., Starnes, C.,
 Scully, S., Guo, J., Elliott, G., McNinch, J., Freeman, D., Shaklee, C.,
 Mann, F., Simone, S., Boone, T. and Chang, M.-S.
 Direct Submission
 TITLE Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive,
 Thousand Oaks, CA 91320, USA
 JOURNAL Location/Qualifiers
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 LOCUS AX205024
 DEFINITION Sequence 1 from Patent WO0155172.
 ACCESSION AX205024
 VERSION AX205024.1 GI:15394259
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1
 Elson, G., Gauchat, J.F., Plun-Favreau, H., Chevalier, S. and Gascan, H.
 Isolated complex comprising a mt-1 protein and in addition at
 least a c1f-1 protein and/or a scntf_gla protein
 Patent: WO 0155172-A 1 02-AUG-2001;
 PIERRE FABRE MEDICAMENT (FR); INSTITUT NATIONAL DE LA SANTE ET DE
 LA RECHERCHE MEDICALE (INSERM) (FR)
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LOCUS AX392089
DEFINITION Sequence 4 from Patent WO0215977.
ACCESSION AX392089
VERSION AX392089.1 GI:19700577
KEYWORDS

SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Senaldi, G.
TITLE Methods and compositions for treating ige-related disease using m
c-1 inhibitors
JOURNAL Patent: WO 0215977-A 4 28-FEB-2002;
Amgen Inc. (US)
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Query Match 100.0%; Score 819; DB 6; Length 819;
Best Local Similarity 100.0%; Pred. No. 1.3e-178;
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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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5	674	82.3	881	6	AX205042
6	669.4	81.7	797	6	AR002595
7	669.4	81.7	797	6	AX392086
8	669.4	81.7	797	6	AF176911
9	654	79.9	1736	9	BC012939
10	627	76.6	1689	9	AF172854
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16	507.2	61.9	258710	2	AR002596
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32	46	5.6	299300	1	AP005026
33	45.2	5.5	125020	9	AF429315
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38	43.2	5.3	6803	9	HS086758
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40	42.4	5.2	1357	9	AF035771
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DEFINITION Sequence 4 from patent US 5741772.
ACCESSION AR002597
VERSION AR002597.1 GI:3964151.
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 819)
AUTHORS Chang, M.-S.
TITLE Neurotrophic factor NNT-1
JOURNAL Patent: US 5741772-A 4 21-APR-1998;
FEATURES Location/Qualifiers

REFERENCE AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 542)
Klm,M.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.Y., Cheong,J.E., Sohn,H.Y., Kim,J.W., Park,H.S., Klm,S. and
Y.K.S.
21C Frontier Korean EST Project 2001
Unpublished
Contact: Klm YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 9 row: G column: 05
High quality sequence, atop: 542.

BASE COUNT	92 a	202 c	155 g	92 t	1 others
ORIGIN					

Query March	54.3%;	Score 445;	DB 12;	Length 542;
Best Local Similarity	90.8%;	Pred. No. 6.4e-88;		
Matches 496;	Conservative	0;	Mismatches 46;	Indels 4;
				Gaps 2

Oy	13	TTGGCCGGAGCCGCGGGCTCGCCTCCCACTCGGCACGCTCTGGAGAGAGACCGCGCC	72
Db	1	TTGCCGGAGCCGCGGGCTCGCCTCAC--TCGCAgCTCCGGAGAGAGCCGACCC	57
Oy	73	GGCCGGCCCGGCCCCAGCCCATGACTCCGAGCAGGGAGCTCGTGGGGATGTTAGC	132
Db	58	GGCGGGCCCGG-CCCAGGCCCATGACTCCGAGCAGGGAGCTCGTGGGGATGTTAGC	116
Oy	133	TTGCCATGCAAGGTGTGTGTGCACCTCCCTGACAGTGCCAGCTCTTAATGCAAGAGAGA	192
Db	117	GTGCTGTGACAGGTGTGTGTGCACCTCCCTGACAGTGCCAGCTCTTAATGCAAGAGAGA	176
Oy	193	TCAGAGCCCTGGCCCTCCATTCAGAAAAACCTATGACTCACCCGTACTGTGAGATCA	252
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Oy	253	ACTCCGACGTTAGGCTGGGACCTTACCTGAACTACCTGGGGGCCCTTTCAAGAGCTGA	312
Db	237	ACTCCGACGTTGGCTGGGACCTATCTGAATTAACCTGGGCCCTTTTCAAGAGCTGAA	296
Oy	313	CTTCAATCCTCTCTGACCTGGGGGCAAACTGTGCCAGAGGCCACGGTCAACTTGAAGT	372
Db	297	CTTCAACCTCCCCGCTGGGGGCAAGACTGTGCCAGAGGCCACGTGTGAATTGAGGT	356
Oy	373	GTGGCGAAGCTCAATGACAGGCTGGGCTGAACCCAGAACTATGAGGCGTACAGTCACT	432

Db 357 GTGGCCAAAGCTCAATGACAAACTGGGGCTAACCAGAACTACAGAGCTTACAGCCACT 416

Qy 433 CCTGTGTACTTGGCGTGGCTTCAAACCGTCAGAGCTGGCCACAGCTGAATCCGACGTAGCCT 492

Db 417 TCTGTGTACTTGGCGTGGCTTCAAACCGTCAGAGCTGGCCACAGCTGTAGCTGGCGCGACCT 476

Qy 493 GGGCCACTTCTGTACAGGCTTCAGAGGCTCTGGGCGACATTTGCAGGTGTACTGGGAC 552

Db 477 GGGCCACTTCTGCACCAAGCTTCAGAGGCTCTGCTGGGACGCAATTGGGGCGTCAATGGAGC 536

Qy 553 GCTTGG 558

Db 537 TCTGGG 542

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Job time : 2214.2 secs
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Query Match 54.7%; Score 448; DB 13; Length 448;
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Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTAGCTGGGAGCTTACTGAACTAAGTGGGGCCCCCTTTCAAGAGAGCTTGCAATCC 60
QY 322 TCTCTGAGTGGGGGAGAACTCTGCGCAGGGGCGACGGTCACTTGAAGTGGGGAG 381
DB 61 TCTCTGAGTGGGGGAGAACTCTGCGCAGGGGCGACGGTCACTTGAAGTGGGGAG 120
QY 382 CCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGGCTGACCTCTGTGTTA 441
DB 121 CCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGGCTGACCTCTGTGTTA 180
QY 442 CTTCGCTGGCTCAACCTGTCAGGCTGCGCAGAGTGAATCTCCAGTACCTGGCCCACTT 501
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QY 502 CTGTACAGAGCTTCAGGGGCTGCTGGGCGACATTGAGGTGATGGCGACCTTGAGTCA 561
DB 241 CTGTACAGAGCTTCAGGGGCTGCTGGGCGACATTGAGGTGATGGCGACCTTGAGTCA 300
QY 562 CCCACTGCCCCAGCCTCTGCGCAGAGGAGCTGAGCCAGGCTGCGCCCTGCGCCCAAG 621
DB 301 CCCACTGCCCCAGCCTCTGCGCAGAGGAGCTGAGCCAGGCTGCGCCCTGCGCCCAAG 360
QY 622 TGAATCTCTCCAGAGATGATGATCTTGTGGCTGCTGAAAGAGCTGCAGACTCTGGTATG 681
DB 361 TGAATCTCTCCAGAGATGATGATCTTGTGGCTGCTGAAAGAGCTGCAGACTCTGGTATG 420
QY 682 GGGTCAGGCAAGAGCTTCAACCGGCTT 709
DB 421 GGGTCAGGCAAGAGCTTCAACCGGCTT 448
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RESULT 14
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DEFINITION mRNA sequence.
ACCESSION BM841897
VERSION BM841897.1 GI:19198306
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 522)
Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,
Oh K.J., Cheong D.E., Sohn H.Y., Kim J.M., Park H.S., Kim S. and
Kim Y.S.
21C Frontier Korean EST Project 2001
TITLE Unpublished
JOURNAL Contact: Kim YS
COMMENT Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
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Location/Qualifiers
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/note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI. The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then deacapped with tobacco acid
pyrophosphatase (TAP). The deacapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

BASE COUNT 90 a 195 c 148 g 89 t
ORIGIN

Query Match 54.6%; Score 447; DB 12; Length 522;
Best Local Similarity 92.2%; Pred. No. 2.3e-88;
Matches 482; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

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DB 1 CTCCCACTCCGACGCTCTCCGAGAGAGAGCCGCGCCGCGCCGCGCCCGCCAGCCCC 59
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DB 180 CAGAAACCTATGACCTCAACCCGCTACCTGAGAGATCACTCCGAGCTTATGAGGACC 239
QY 275 TACCTGAATCACTGGGGGCCCCCTTTCAACGAGCTGATCTTCAATCTCTGAGCTGGG 334
DB 240 TACCTGAATCACTGGGGGCCCCCTTTCAACGAGCTGATCTTCAATCTCTGAGCTGGG 299
QY 335 GAGAAATCTGCCCCAGGGGCGACGCTCACTTGAAGTGTGGCGAAGCTCAATGACAG 394
DB 300 GAGAAATCTGCCCCAGGGGCGACGCTCACTTGAAGTGTGGCGAAGCTCAATGACAG 359
QY 395 CTGGGAGCTGACCCAGAACTATGAGGCGTACAGTCACTCTGTGTACTTGGTGGCCCTC 454
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QY 455 AACCGTCAAGCTGCCAGAGCTGAACCTCCAGCGTACCTGGCCCACTTGTATGACAGCTTC 514
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RESULT 15
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LOCUS K-EST0089713 S19N665307 Homo sapiens cDNA clone S19N665307-9-G05
DEFINITION 5', mRNA sequence.
ACCESSION BM821005
VERSION BM821005.1 GI:19177418
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DE	Homo sapiens mRNA; EST DKFZp779H1332_r1 (from clone DKFZp779H1332)
XX	EST; expressed sequence tag.
KX	
OS	Homo sapiens (human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX	
RN	[1]
RP	1-634
RA	Outenwaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weill B.,
RA	Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RT	Submitted (07-MAY-2003) to the EMBL/Genbank/DBD databases.
RL	MIR5, Ingolstedter Landstr.1, D-85764 Neuberg, GERMANY
XX	
CC	This is the 5' sequence of the clone insert
CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC	sequenced by MediGenomix (Marinried/Germany) within the cDNA
CC	sequencing consortium of the German Genome Project.
CC	No SI sequence available.
CC	This clone (DKFZp779H1332) is available at the RZPD in Berlin.
CC	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC	14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX	
PH	Key
PH	Location/Qualifiers
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FT	/clone="DKFZp779H1332"
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FT	DH10B; sites SfiI + SfiIb"
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	Best Local Similarity 88.7%; Pred. No. 5.2e-93;
	Matches 540; Conservative 0; Mismatches 65; Indels 4; Gaps 3;
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Db	26 AGGGAGCTCGTGGGGAGTGTAGTCTTGTGACAGGCTGTGGACCTCCCTGAGT 85
OY	169 GCCAGCTTTATGCGACAGAGATCCAGGCCCTCGGCCCTTCATCCAGAAACCTATGA 228
Db	86 GCCAGCTTTATGCGACAGAGATCCAGGCCCTCGGCCCTTCATCCAGAAACCTATGA 145
OY	229 CCTGACCCGCTAACCTGAGCATCAACTCCGAGCTTAGCTGGAGCTTACCTGAACCTACT 288
Db	146 CCTGACCCGCTAACCTGAGCATCAACTCCGAGCTTAGCTGGAGCTTACCTGAACCTACT 205
OY	289 GGGGCCCCCTTCAACGAGCTGACTTCATCTCTTGACCTGGGGGACAGAACTTGCC 348
Db	206 GGGGCCCCCTTCAACGAGCTGACTTCATCTCTTGACCTGGGGGACAGAACTTGCC 265
OY	349 CAGGGCCACGGTCAACTTGGAAAGTGTGGCCAGAACTTCATATACAGCTTGCGGCTGACCA 408
Db	266 CAGGGCCACGGTCAACTTGGAAAGTGTGGCCAGAACTTCATATACAGCTTGCGGCTGACCA 325
OY	409 GAACCTATGAGCGTACAGTCACTCCGTGTGTTACTTGGTGGGCTCAACGCTGAGGCTGC 468
Db	326 GAACCTATGAGCGCTACAGCCACTTCTGTGTGTTACTTGGTGGGCTCAACGCTGAGGCTGC 385
OY	469 CACAGCTGAATCTCGACGTAGCTGGGCCCACTTCTGTATACAGCC--TCCAGGGGCTGCTG 526
Db	386 CACGTGTGAGCTGGGCGGACGCTGGGCCCACTTCTGTATACAGCCCTCCAGGGGCTGCTG 445
OY	527 GGCAGCATTT-GCAGGTGTATGCGGAGCGCTTGGCTACCACTGCCCAAGCTCTTGCC-AG 584

Db		446	GGCANAATTGGCGGAGCGTCAATGGACGCTTGAGGCTAACCCACTGCCCCAAGCCGCTGCTGG	505
Oy		585	GGACTGAACCAGCCTGGGCCCTGTGGCCCCTGCCCCACAGTAGACTTCCTCCAGAAGATGATG	644
Db		506	GGACTGAACCCACTTGGACTCTCTGGCCCTGGCCACAAGTAGACTTCTTCANNAATAATGACG	565
Oy		645	ACTTTGGCTGCTGAAGAGCTGCAGACCTTGCTATAGGCGTTTCAGCCAGAAGACTTCAAC	704
Db		566	ACTTGTGGCTGCTGAAGAGCTGCAGACCTTGCTATAGGCGCTGCGCCAGAAGACTTCAAC	625
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Db		626	GGCTCAAGA	634

RESULT 12	BMB46370	532 bp	mRNA	linear	EST 06-MAR-2002
LOCUS	BMB46370				
DEFINITION	K-EST0125376 S13KMS5S1 Homo sapiens cDNA clone S13KMS5S1-21-A09 5'				
ACCESSION	BMB46370				
VERSION	BMB46370.1	GI:19202769			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,				
JOURNAL	Oh,K.T., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and				
COMMENT	Kim,Y.S.				
	21C Frontier Korean EST Project 2001				
	Unpublished				
	Contact: Kim YS				
	Genome Research Center				
	Korea Research Institute of Bioscience & Biotechnology				
	52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea				
	Tel.: +82-42-860-4470				
	Fax: +82-42-860-4409				
	Email: yongsung@mail.kribb.re.kr				
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	(A) + RNA was dephosphorylated with bacterial alkaline				
	phosphatase (BAP) and then decapped with tobacco acid				
	pyrophosphatase (TAP). The decapped intact mRNA was				
	ligated with DNA-RNA linker including EcoR I site by				
	treatment of T4 RNA ligase and the first strand cDNA was				
	synthesized from oligo dT-selected mRNA by priming with				
	dT-tailed vector. The dT-called vector was adjusted to				
	have about 60nt. The cDNA vector was circularized with E.				
	coli DNA ligase after digestion of EcoR which site is				
	also included in vector. An RNA strand converted to a DNA				
	strand by Okayama-Berg method. The obtained cDNA vectors				
	were used for transformation of competent cells E. coli				
	Top10F by electroporation method. The cDNA libraries				
	constructed by this method are full-length enriched cDNA				
	library. After analyzing and sequencing about 2,000 ~				
	3,000 colonies in original cDNA library, the abundant				
	cDNAs were selected and amplified by PCR reaction using				
	vector region primer including T7 promoter as 5' primer				
	and N(dT)14 as 3' primer. The PCR products were used as				

3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

93 a 165 c 126 g 92 t

ORIGIN

Query Match 58.1%; Score 476; DB 10; Length 476;
Best Local Similarity 100.0%; Pred. No. 9e-95;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

203 GGGCCCTCATCAGAAAACCTATGACCTACCGGCTACCTGAGATCAATCCGAGC 262
1 GGGCCCTCATCAGAAAACCTATGACCTACCGGCTACCTGAGATCAATCCGAGC 60
263 TTAGCTGGAGCTACCTGATGACTGAGGCCCCCTTTCACAGAGCTGACTTCAATCT 322
61 TTAGCTGGAGCTACCTGATGACTGAGGCCCCCTTTCACAGAGCTGACTTCAATCT 120
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121 CCTGCACTGGGGGAGAAAACCTTGTCCAGAGGCCACAGCTCACTTGAAGTGGCGAAGC 180
383 CTGATGACAGGCTGGGCTGACCCAGAACCTATGAGGCGGTACAGTCACTCTGTGTAC 442
181 CTGATGACAGGCTGGGCTGACCCAGAACCTATGAGGCGGTACAGTCACTCTGTGTAC 240
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241 TTGCGTGGCTCAACCGCTCAGGCTGACAGCTGAACTCGAGCTGAGCTGGCCCACTTC 300
503 TGTACAGCTTCCAGGAGCTTGTGGGACAGTTCAGAGTGTATGAGCGACGCTTGGCTAC 562
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563 CCAGTGGCCAGGCTTGTGCAAGGAGCTGAGGAGCTGGGCCCCCTGGCCCAAGT 622
361 CCAGTGGCCAGGCTTGTGCAAGGAGCTGAGGAGCTGGGCCCCCTGGCCCAAGT 420
623 GACTTCTCTCAGAGATGATGATCTTGTGGCTGTGAGAGAGCTGACAGCTGGCT 678
421 GACTTCTCTCAGAGATGATGATCTTGTGGCTGTGAGAGAGCTGACAGCTGGCT 476

RESULT 10

AL543945

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL543945 1028 bp mRNA linear EST 31-MAY-2003
AL543945 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
Clone CS0D1004YM15 5-PRIME, mRNA sequence.
AL543945 GI:31265790
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1028)
Ll.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12876424.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr; Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6127.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1004AG08QPl&cluster=6127.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/InvitrogenCorporation1600
Faraday Avenue Genoscope sequence ID : CS0D1004AG08QPl.
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source

BASE COUNT

190 a 339 c 283 g 212 t

ORIGIN

Query Match 57.8%; Score 473.4; DB 9; Length 1028;
Best Local Similarity 88.5%; Pred. No. 4.3e-94;
Matches 525; Conservative 0; Mismatches 66; Indels 2; Gaps 1;

191 GATCAGGCTCTGGCCCTCCATCCAGAAAACCTATGACCTGACCTGAGGAT 250
41 GGTAACGGTCCGGAATTCGCCGAGTAGAAAACCTATGACCTGACCTGAGGAT 100
251 CAATCCGAGCTTACCTGAGGAGCTGACCTGAACTACCTGAGGAGGCCCCCTTTCACAGAGCT 310
101 CAATCCGAGCTTACCTGAGGAGCTGACCTGAACTACCTGAGGAGGCCCCCTTTCACAGAGCT 160
311 GACTTCAATCTCTGCACTGAGGAGGAGAAAACCTGAGCCAGAGGCGACAGTCACTTGGAA 370
161 GACTTCAATCTCTGCACTGAGGAGGAGAAAACCTGAGCCAGAGGCGACAGTCACTTGGAA 220
371 GTTGGGAGAGCTTCAATGACAGGCTGAGGCTGACCCAGAACTATGAGGCGTACAGTAC 430
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HSM090574

ID

HSM090574

standard; RNA; EST; 634 BP.

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XX BX497225.1

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XX

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XX

XX

XX

XX

XX

XX

XX

XX

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 K-EST0118015 S13KMS5 Homo sapiens cDNA clone S13KMS5-35-D11 5',
 mRNA sequence.

ACCESSION BM840863
 VERSION BM840863.1 GI:19197272

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 573)
 Oh,K.N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Kim,Y.S., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished
 COMMENT Contact: Kim YS

Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
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 High quality sequence stop: 573.
 Location/Qualifiers

FEATURES source

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 /note="Vector: pcns; Site 1: EcoRI; Site 2: NotI; The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then dephosphorylated with tobacco acid
 pyrophosphatase (TAP). The dephosphorylated mRNA was
 ligated with DNA-RNA linker including EcoR I site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dT-selected mRNA by priming with
 dT-tailed vector. The dT-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10F by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

BASE COUNT 98 a 217 c 160 g 98 t
 ORIGIN

Query Match 59.2%; Score 485.2; DB 12; Length 573;
 Best Local Similarity 91.5%; Pred. No. 9e-97;
 Matches 525; Conservative 0; Mismatches 48; Indels 1; Gaps 1;

QY 35 CTCCTCCAGCTCCGAGCTCTGGAGAGAGCCGCGCCCGGCCCCCAAGCCCC 94
 DB 1 CTCCTCCAGCTCCGAGCTCTGGAGAGAGCCGCGCCCGGCCCCCAAGCCCC 59
 QY 95 ATGAGACTCCGAGGAGGAGCTCTGGAGAGAGCTCTGGAGAGCTCTGGAGAG 154
 DB 60 ATGAGACTCCGAGGAGGAGCTCTGGAGAGAGCTCTGGAGAGCTCTGGAGAG 119

QY 155 CACCTCCCTGACAGTCCAGCTCTTAATGACAGAGATTCAGACCCCTGACCTC 214
 DB 120 CACTCCCTGACAGTCCAGCTCTTAATGACAGAGATTCAGACCCCTGACCTC 179
 QY 215 CAGAAACTATGACTCTACCCGCTTACCTGAGACATCACTCCGAGCTTAGTGGACC 274
 DB 180 CAGAAACTATGACTCTACCCGCTTACCTGAGACATCACTCCGAGCTTAGTGGACC 239
 QY 275 TACCTGAACATCCTGGAGGCCCCCTTCAAGAGCCGAGCTTCAATCTCTGAGCGGG 334
 DB 240 TATCTGAACATCCTGGAGGCCCCCTTCAAGAGCCGAGCTTCAATCTCTGAGCGGG 299
 QY 335 GCAGAAACTCTGCCAGGAGCAAGCTTCACTTGAAGTGTGAGGAGCTTCAATGACAG 394
 DB 300 GCAGAAACTCTGCCAGGAGCAAGCTTCACTTGAAGTGTGAGGAGCTTCAATGACAG 359
 QY 395 CTGCGGCTGACCCAGAGACTATGAGGCGTACAGTCTCTGTTTACTTGGCTGGCCTC 454
 DB 360 CTGCGGCTGACCCAGAGACTATGAGGCGTACAGTCTCTGTTTACTTGGCTGGCCTC 419
 QY 455 AACCTGACAGCTGCCAGCTTCACTTGAAGTGTGAGGAGCTTCAATGACAGCTC 514
 DB 420 AACCTGACAGCTGCCAGCTTCACTTGAAGTGTGAGGAGCTTCAATGACAGCTC 479
 QY 515 CAGGCTCTGCTGGGAGCAATTCAGAGTGTGAGGAGCTTCAATGACAGCTC 574
 DB 480 CAGGCTCTGCTGGGAGCAATTCAGAGTGTGAGGAGCTTCAATGACAGCTC 539
 QY 575 CCTCTGCCAGGACTGACCGCCTGGGCCCCCTGGCCCTG 608
 DB 540 CCGCTGCTGGAGCTGAAACCACTTGGACTCTGGCCCTG 573

RESULT 9 BE632644

LOCUS uv63f01.y1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:3411865
 DEFINITION 5', mRNA sequence.

ACCESSION BE632644
 VERSION BE632644.1 GI:9915332
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 476)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rmail.nih.gov
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1087677

Seq primer: -40R from Gibco
 High quality sequence stop: 464.
 Location/Qualifiers

FEATURES source

1..476
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:3411865"
 /sex="male"
 /tissue_type="Spleen"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares mouse 3NDMS"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5']
 TGTATCAATCTGAAGTGGAGCGCGCGCTGTTTTTTTTTTTTTTTTTTTTTTTT

Db 218 GGGCCCCCTTTCAACGAGCCAGACTCAACCTCCCGCTGGGGGAGAGACTCTGCC 297
Qy 349 CAGGGCCACGCTCACTTGGAGTGTGGAGAGCTTCAATGACAGCTGGGCTACCA 408
Db 298 CAGGGCCACGCTTGGAGTGTGGAGAGCTTCAATGACAGCTGGGCTACCA 357
Qy 409 GAACATGAGAGGCTGACAGCTCACTCTGTTACTTGGCTGAGCTCAACCTGAGCTGC 468
Db 358 GAACATGAGAGGCTTCAACGCTTCTGTTACTTGGCTGAGCTCAACCTGAGCTGC 417
Qy 469 CACAGCTGATCTCGACGCTGAGCTTCTGTTACTTGGCTGAGCTCAACCTGAGCTGC 528
Db 418 CACTCTGAGCTGCGCCGAGCTGAGCTTCTGTTACTTGGCTGAGCTCAACCTGAGCTGC 477
Qy 529 CAGCATTCAGGCTGATGAGCTGAGCTTGGCTGAGCTTCTGTTACTTGGCTGAGCTGC 588
Db 478 CAGCATTCAGGCTGATGAGCTGAGCTTGGCTGAGCTTCTGTTACTTGGCTGAGCTGC 537
Qy 589 TGAGCCAGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 648
Db 538 TGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597
Qy 649 CTGGCTGCTGAAGAGAGCTGAGCTGAGCTTGGCTGAGCTTCTGTTACTTGGCTGAGCTGC 708
Db 598 CTGGCTGCTGAAGAGAGCTGAGCTTGGCTGAGCTTCTGTTACTTGGCTGAGCTGC 657
Qy 709 TGAAG 766
Db 658 CAAG 717
Qy 767 TTCTGACCTCTGACCTTGAACCCCAACCTGC 799
Db 718 TTCTGACCTCTGACCTTGAACCCCAACCTGC 750

RESULT 4
LOCUS BG164929 1053 bp mRNA linear EST 06-FEB-2001
DEFINITION BG164929.1 NIH_MGC_89 Homo sapiens CDNA clone IMAGE:445813 5',
mRNA sequence.
ACCESSION BG164929
VERSION BG164929.1 GI:12671563
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL10244 row: m column: 14
High quality sequence start: 3
High quality sequence stop: 675.
Location/Qualifiers

FEATURES

source
1. 1053
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:445813"
/issue_type="hyperphicoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH_MGC_89"
/note="Organ: kidney; Vector: pCMV-Sport6; Site_1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library.
BASE COUNT 210 a 351 c 292 g 200 t

Query Match 66.4%; Score 544; DB 10; Length 1053;
Best Local Similarity 88.2%; Pred. No. 1.2e-109;
Matches 660; Conservative 0; Mismatches 80; Indels 8; Gaps 6;

Qy 24 CGCGGCTGCGCTCCCACTCCGAGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 83
Db 2 CGCGGCTGCGCTCCCACTCCGAGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 61
Qy 84 CCCCAGCCCATGAGCTCTCGAG 143
Db 62 CCCCAGCTCCCATGAGCTCTCGAG 121
Qy 144 CGGAGCTGAGACCTCCGAG 203
Db 122 CGGAGCTGAGACCTCCGAG 181
Qy 204 GCCCTCCATCCAG 263
Db 182 GCCCTCCATCCAG 241
Qy 264 TAGCTGAG 319
Db 242 TAGCTGAG 301
Qy 320 CCTCCTGAG 378
Db 302 CCTCCTGAG 361
Qy 379 AAGCTCAATGAG 438
Db 362 AAGCTCAATGAG 421
Qy 439 TTACTTGGCTGAG 498
Db 422 TTACTTGGCTGAG 481
Qy 499 CTTCTGAG 558
Db 482 CTTCTGAG 541
Qy 559 CTACCACTG-CGCCAGCTCTGAG 616
Db 542 CTACCACTG-CGCCAGCTCTGAG 601
Qy 617 CACAGTGAATCTCTCCAG 676
Db 602 CACAGTGAATCTCTCCAG 661
Qy 677 CTATGAGCTTCAAG 736
Db 662 CTGAGGCTGAG 720
Qy 721 TCAGTCACTCTGAG 764
Db 721 GCAGTCACTCTGAG 748

RESULT 5
LOCUS BG437538 853 bp mRNA linear EST 14-MAR-2001
DEFINITION BG437538.1 NIH_MGC_18 Homo sapiens CDNA clone IMAGE:4621530 5',
mRNA sequence.
ACCESSION BG437538
VERSION BG437538.1 GI:13344044
KEYWORDS EST.
SOURCE Homo sapiens (human)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comogen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 06:10:21 ; Search time 2211.2 Seconds
(without alignments)
9002.070 Million cell updates/sec

Title: US-09-931-704-4

Perfect score: 819
Sequence: 1 tatataaagcttcgcgcg.....agcccaagcagctgtgctt 819

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc1:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc1:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hnv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	671.4	82.0	678	14	BY735168 BY735168
2	644.4	78.7	887	13	BQ948158 AGENCOURT
3	568.6	69.4	1157	13	BQ940483 AGENCOURT
4	544	66.4	1053	10	BG164929 BG164929 602343555

5	54.3	66.3	85.3	10	BG437538
6	504.6	61.6	584	12	BM763333
7	491.2	60.0	590	12	BM848189
8	485.2	59.2	573	12	BM840863
9	476	58.1	476	10	BM832644
10	473.4	57.8	1028	9	AL543945
11	468.2	57.2	634	2	HSW090574
12	455.4	55.6	532	12	BM846370
13	448	54.7	448	13	BY531444
14	447	54.6	522	12	BM841897
15	445	54.3	542	12	BM821005
16	441.4	53.9	529	12	BM847924
17	414	50.5	831	29	CC138171
18	407.6	49.8	569	12	BM846748
19	390.4	47.7	505	4	BX528877
20	381.4	46.6	388	13	BY022718
21	377.8	46.1	458	12	BM363136
22	363	44.3	668	14	BY734701
23	351.2	42.9	420	12	BM764238
24	351	42.9	354	13	BY015239
25	333.6	40.7	512	9	AI390475
26	329.8	40.3	482	12	BM846622
27	312.4	38.1	407	9	AI752561
28	295.8	36.1	392	13	BY012378
29	278.4	34.0	663	14	BY722568
30	263	32.1	281	10	BB864730
31	261.2	31.9	488	9	AA015243
32	257	31.4	359	13	BY009925
33	255.8	31.2	377	13	BY017916
34	252.2	30.8	473	14	CB729926
35	251.2	30.7	357	13	BY185798
36	246.8	30.1	552	10	BG095271
37	228.4	27.9	440	10	BG148676
38	228	27.8	385	13	BY018063
39	228	27.8	913	12	BI912197
40	186	22.7	681	9	AL857796
41	172.8	21.1	915	10	BF035982
42	155.8	19.0	560	9	AL800340
43	151.8	18.5	617	9	AL959824
44	151.8	18.5	659	9	AL865000
45	128.8	15.7	381	13	BY093116

ALIGNMENTS

RESULT 1
BY735168
LOCUS
DEFINITION
BY735168 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) CDNA Mus musculus cDNA clone G330015622 5', mRNA
Sequence.
ACCESSION
BY735168
VERSION
BY735168.1 GI:27148295
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 678)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oshio, N., Saito, R., Suzuki, H., Yamnaka, I., Kiyosawa, H.,
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogi, A., Schonbach, C.,
Gojobori, T., Baldarelli, R., Hill, D.P., Bull, C., Hume, D.A.,
Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,
Beisel, K.W., Blake, J.A., Brad, D., Brusic, V., Chochia, C., Corbani,
L.E., Cousine, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest,
A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
Gough, J., Grimmond, S., Guenichon, S., Hirokawa, N., Jackson, I.J.,
Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M.,
Kling, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons,
P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mikl,
H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G.,

CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.

XX Sequence 768 BP; 137 A; 278 C; 217 G; 136 T; 0 other;

Query Match 80.6%; Score 660; DB 22; Length 768;
 Best Local Similarity 92.1%; Pred. No. 4.3e-156;
 Matches 707; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 2 ATTATTAAGCTTGGCGGAGCGCGCTGCGCCCTCCCACTCCGACGCTCTGGAGAG 61
 DB 2 ATTATTAAGCTTGGCGGAGCGCGCTGCGCCCTCCCACTCCGACGCTCTGGAGAG 61
 QY 62 GAGCCG 121
 DB 62 GAGCCG 120
 QY 122 GGGATGTAGCTTGGCTTATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTTAA 181
 DB 121 GGGATGTAGCTTGGCTTATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTTAA 180
 QY 182 CGCAGCAGAGATTCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAC 241
 DB 181 CGCAGCAGAGATTCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAC 240
 QY 242 CTGAGCATCACTCCGAGCTTATGAGGAGACCTTACCTGAGGAGCGCGCTTTC 301
 DB 241 CTGAGCATCACTCCGAGCTTATGAGGAGACCTTACCTGAGGAGCGCGCTTTC 300
 QY 302 AACGAGCTGACTTCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
 DB 301 AACGAGCTGACTTCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 362 AACTTGAAGTGTGGGAGAGCTTCATGACAGGCTGCTGCTGCTGCTGCTGCTGCTG 421
 DB 361 AACTTGAAGTGTGGGAGAGCTTCATGACAGGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 422 TACAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
 DB 421 TACAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 482 CGACGTAGCTGAGCCCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
 DB 481 CGACGTAGCTGAGCCCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 542 GTCATGTGCGACGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
 DB 541 GTCATGTGCGACGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 602 GCG 661
 DB 601 GCG 660
 QY 662 GAGCTGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 721
 DB 661 GAGCTGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 722 CAGCTTCCAGCAGCTTCACTGCACTGCACTTGGAGGAGCACTGCTTTC 769
 DB 721 CAGCTTCCAGCAGCTTCACTGCACTGCACTTGGAGGAGCACTGCTTTC 768

RESULT 12

AAAB8547
 ID AAAB8547 standard; DNA; 648 BP.

XX AAAB8547;

AC 22-JAN-2001 (first entry)

XX Mouse Interleukin-B60 (IL-B60) gene.

KW Interleukin-B60; IL-B60; mouse; cytokine; cytokine-like factor-1;
 KW haematopoietic; inflammation; antiinflammatory; autoimmune disease;
 KW therapy; ds.

XX Mus musculus.

Key	Location/Qualifiers
FT CDS	1..648
FT sig_peptide	/*tag= a
FT mat_peptide	1..51
FT	/*tag= b
FT	52..645
FT	/*tag= c

PN MO200053631-A1.

PD 14-SEP-2000.

XX 09-MAR-2000; 2000MO-US06182.

XX 11-MAR-1999; 99US-0267901.

XX (SCHE) SCHERING CORP.

XX Opmann B, Timans JC, Kastellein RA, Bazan JF;

XX WPI; 2000-587426/55.

XX P-PSDB; AAB19587.

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
 PT polypeptides, and nucleic acids, useful in research, diagnosis and for
 PT treating inflammatory and autoimmune disorders -

XX Claim 17; Page 17; 97pp; English.

XX The present sequence is that of DNA encoding mouse interleukin-B60
 CC (IL-B60, see AAB19587), a novel, small soluble cytokine-like protein
 CC of 215 amino acids that exhibits structural motifs characteristic
 CC of a member of the long-chain cytokines, and which shows homology
 CC to granulocyte colony stimulating factor and interleukin-6. IL-60B
 CC may have either stimulatory or inhibitory effects on haematopoietic
 CC cells, including e.g. lymphoid cells, such as T-cells, B-cells,
 CC natural killer cells, macrophages, dendritic cells, haematopoietic
 CC progenitors, etc. Methods are provided for modulating the
 CC physiology or development of a cell or tissue culture cells by
 CC contacting the cell with an agonist or antagonist of IL-B60 or an
 CC agonist of antagonist of a complex of mature IL-B60 and its
 CC partner, cytokine-like factor-1 (CLF-1, see AAB19588). The
 CC IL-B60/CLF-1 cytokine serves as a key physiological factor in motor
 CC neuron development and regeneration. IL-60B, its agonists and
 CC antagonists may be used to treat inflammatory or autoimmune
 CC disorders and also for drug screening.

XX Sequence 648 BP; 130 A; 217 C; 170 G; 131 T; 0 other;

Query Match 78.9%; Score 646.4; DB 21; Length 648;
 Best Local Similarity 99.8%; Pred. No. 1.1e-152;
 Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 125 ATGTAGCTTGGCTTATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTTATGCG 184
 DB 1 ATGTAGCTTGGCTTATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTTATGCG 60

QY 185 ACAGAGATCCAGGCGCTGCGCCCTCCATCCAGAAACCTATGACCTACCGGCTACCTG 244
 DB 61 ACAGAGATCCAGGCGCTGCGCCCTCCATCCAGAAACCTATGACCTACCGGCTACCTG 120

QY 245 GAGCATCACTCCGAGCTTATGCTGAGCTTACCTGGAACCTACCTGCGGCGCCCTTTCAAC 304
 DB 121 GAGCATCACTCCGAGCTTATGCTGAGCTTACCTGGAACCTACCTGCGGCGCCCTTTCAAC 180

QY 305 GAGCTGACTTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364

CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
CC occurring variant, and diagnosing an IGE-related disease or
CC susceptibility of an IGE-related disease based on the presence or amount
CC of expression of the polypeptide and a pharmaceutical composition for use
CC in treating IGE-related disease, comprising the NNT1 inhibitor.
CC The NNT1 inhibitor is useful for preventing and treating IGE-related
CC disease, modulating IGE levels, and creating allergic diseases e.g.
CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,
CC pollinosis, asthma, immune diseases and disorders, diseases involving
CC abnormal cell proliferation including cancer, arteriosclerosis and
CC vascular stenosis, diseases and conditions relating to dysfunction of
CC immune system including rheumatoid arthritis, psoriatic arthritis,
CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,
CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
CC bowel disease, transplant rejection, and graft versus host disease, and
CC reproductive diseases and disorders including infertility, miscarriage,
CC preterm labour and delivery, and endometriosis. The present sequence
CC encodes human NNT1.
XX
XX

SO Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;

Query Match 81.7%; Score 669.4; DB 24; Length 797;

Best Local Similarity 92.0%; Pred. No. 1.9e-158;

Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

5 ATTAAGCTTGGCCGAGCGCGGCTCCGCTCCCACTCCGCGCAGCTCTGGAGAGAGAG 64
1 ATTAAGCTTCCCGAGCGCGGCTCCGCTCCCACTCCGCGCAGCTCTGGAGAGAGAG 60
65 CCGCGCCCG 124
61 CCGGACCG 119
135 ATGTTAGCTTGGCTATGACCGGTGCTGTGGGACCTTCCCTGAGTGGCAGCTTTAATGC 184
120 ATGTTAGCGTGTCTGTGCAACGGTGTCTGTGCACTTCCCTGAGTGGCAGCTTTAATGC 179
185 ACAGGAGATCCAGGCG 244
180 ACAGGAGATCCAGGCG 239
245 GAGCATCACTCCGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 304
240 GAGCATCACTCCGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 299
305 GAGCTGACTTCAATCTCTCTGACTGGGGGCAAGAACTTGGCCAGGCGCGCGCGCGCG 364
300 GAGCTGACTTCAATCTCTCTGACTGGGGGCAAGAACTTGGCCAGGCGCGCGCGCGCG 359
365 TTGGAAGTGGGGAAGCTCAATGACGCTGGCGCTGACCCAGAACTATGAGCGCTAC 424
360 TTGGAAGTGGGGAAGCTCAATGACGCTGGCGCTGACCCAGAACTATGAGCGCTAC 419
425 AGTCACTCTCTGTACTTGTGCTGAGCTCAACCGTCAAGCTGCAAGCTGAACCTGCA 484
420 AGTCACTCTCTGTACTTGTGCTGAGCTCAACCGTCAAGCTGCAAGCTGAACCTGCA 479
485 CGTACCTGGGCCCACTTCTGTACAGAGCTTCAAGGCTGTGGGGCAAGCTTGAAGTGC 544
480 CGTACCTGGGCCCACTTCTGTACAGAGCTTCAAGGCTGTGGGGCAAGCTTGAAGTGC 539
545 ATGGGAGAGCTTGGGCAAGCTCAAGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 604
540 ATGGGAGAGCTTGGGCAAGCTCAAGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 599
605 CTTGGCGCTTCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 664
600 CTTGGCGCTTCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 659
665 CTGAGAGCTTGGGCTATGGGCTTCAAGGAACTTCAACCGGCTTGAAGAAATGACAG 724
660 CTGAGAGCTTGGGCTATGGGCTTCAAGGAACTTCAACCGGCTTGAAGAAATGACAG 719

Oy 725 CCTCAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 783
Db 720 CCTCAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 778

RESULT 11

AAH99772 standard; cDNA; 768 BP.

AAH99772;

16-OCT-2001 (first entry)

Human protein encoding cDNA sequence SEQ ID NO:607.

Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antifungal; antihypertensive; antirheumatic; antitubercular; antitumor;
antibacterial; endocrine; cardiac; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;
dermatological; antiallergic; antiaesthetic; antidiabetic; cytostatic;
neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
immunomodulatory; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
genetic disease; haematopoietic disorder; platelet disorder; asthma;
chromocytogenesis; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
neurological disorder; ss.

Homo sapiens.

WO200153455-A2.

26-JUL-2001.

22-DEC-2000; 2000WO-US35017.

23-DEC-1999; 99US-0471275.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

(HYSE-) HYSBO INC.

Tang YF, Liu C, Dmanac RT;

WPI; 2001-457603/49.

P-PSDB; AAM25831.

Isolated human polynucleotides encoding polypeptides, useful for the

treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

Claim 1; Page 638; 1217p; English.

AAH99166 to AAH9904 encode the human proteins given in AAM25225 to
AAM25963. The proteins can have activities based on the tissues and
cells they are expressed in, such as: antineoplastic; antirheumatic;
antiallergic; immunosuppressive; antibacterial; endocrine; cardiac;
central nervous system; virucide; anti-HIV; fungicide; antimutagen;
cardiovascular; antianemic; antidiabetic; antiallergic; antineoplastic;
antitumor; osteoporosis; dermatological; antiallergic; antineoplastic;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antiparkinsonian; and immunomodulatory. The proteins and polynucleotides
encoding them can be used in gene therapy, antisense therapy and vaccine
production. The proteins and polynucleotides are useful for screening for
agonists or antagonists of a protein and for the treatment and diagnosis
of disorders associated with the activity of a protein e.g. inflammation,
rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
infections, autoimmunity, genetic diseases, haematopoietic disorders,
anaemia, platelet disorders, chromocytopenia, wounds, burns, ulcers,
osteoporosis, severe combined immunodeficiency, eczema, allergic

PI Chang M;
XX MPI; 2000-338492/29.
DR P-PSDB; AAY87813.
XX

PT New nucleic acids encoding neurotrophic factors useful for stimulating
PT growth of motor or sympathetic neurons for treating neuron cell damage
XX

PS Claim 1a; Fig 1; 42pp; English.

XX This invention describes a novel nucleic acid molecule (I) encoding a
XX novel neurotrophic factor (NNT-1) (II) which has nootropic,
XX neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
XX ophthalmological activity. (I) is useful for producing NNT-1
XX polypeptides which are useful for treating patients in whom various
XX cells of the central, autonomic, or peripheral nervous system have
XX degenerated and/or have been damaged by congenital disease, trauma,
XX mechanical damage, surgery, stroke, ischemia, infection, metabolic
XX disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
XX proteins are used to treat diseases like Alzheimer's, Parkinson's,
XX amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
XX disease, peripheral neuropathy induced by diabetes or other metabolic
XX disorders, and/or dystrophies or degeneration of the neural retina such
XX as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
XX night blindness, progressive cone-rod degeneration, immune disorders and
XX hematoepithelial disorders. (I) is effective in treating neurological
XX conditions and promotes neuron regeneration. Neural functions are
XX effectively restored in patients suffering from various neurological
XX disorders. This sequence encodes the human NNT-1 protein described in the
XX method of the invention.

XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;

XX Query Match 81.7%; Score 669.4; DB 21; Length 797;
XX Best Local Similarity 92.0%; Pred. No. 1.9e-158;
XX Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 5 ATTAAAGCTTGGCGGAGCGGCGCTCGCCCTCCCACTCGGACGCTCTGGAGAGGAG 64
DB 1 ATTAAAGCTTGGCGGAGCGGCGCTCGCCCTCCCACTCGGACGCTCTGGAGAGGAG 60
QY 65 CCG 124
DB 61 CCGCAACCG 119
QY 125 ATGTTAGCTTGGCTATGCAAGGTGCTGTG3CACTCTCTGCAAGTGCAGCTCTTAATGCG 184
DB 120 ATGTTAGCTTGGCTATGCAAGGTGCTGTG3CACTCTCTGCAAGTGCAGCTCTTAATGCG 179
QY 185 ACAGAGAGATCCAGGCG 244
DB 180 ACAGAGAGATCCAGGCG 239
QY 245 GAGCATCAACTCCGAGCTTAAAGTGGAGCTCACTCACTCACTCACTCACTCACTCACT 304
DB 240 GAGCATCAACTCCGAGCTTAAAGTGGAGCTCACTCACTCACTCACTCACTCACTCACT 299
QY 305 GAGCGCTGACTCACTCTCTGCACTGGGAGGAGAACTCTGCGCCAGGCGCAAGCTCAAC 364
DB 300 GAGCGCTGACTCACTCTCTGCACTGGGAGGAGAACTCTGCGCCAGGCGCAAGCTCAAC 359
QY 365 TTGGAAGTGTGGCGAAGCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGGCTTAC 424
DB 360 TTGGAAGTGTGGCGAAGCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGGCTTAC 419
QY 425 AGTCACCTCTGTGTAATCTTGGCTGAGCTCAACCGCTGAGGCTGAGCTGAGCTGAGCT 484
DB 420 AGTCACCTCTGTGTAATCTTGGCTGAGCTCAACCGCTGAGGCTGAGCTGAGCTGAGCT 479
QY 485 CGTAGCTTGGCGCACTTCTGTATCAAGCTTCAAGGCGCTCTGCGGCGAGCATTTGAGGCTTTC 544
DB 480 CGTAGCTTGGCGCACTTCTGTATCAAGCTTCAAGGCGCTCTGCGGCGAGCATTTGAGGCTTTC 539

QY 545 ATGAGCAGCGCTTGGCTAATCCCACTGCGCCGAGCTTGGCGAGGAGCTGAGCGCTGCGCC 604
DB 540 ATGAGCAGCGCTTGGCTAATCCCACTGCGCCGAGCTTGGCGAGGAGCTGAGCGCTGCGCC 599
QY 605 CCTGCGCGCTGCGCGCAAGTGAATCTTCTCCAGAAAGATGATGACTTGTGCTGTGAAGAG 664
DB 600 CCTGCGCGCTGCGCGCAAGTGAATCTTCTCCAGAAAGATGATGACTTGTGCTGTGAAGAG 659
QY 665 CTGCAAGCTTGGCTATGAGGCTTCAAGGAGCTTCAACCGGCTTAAGAAAGATGAG 724
DB 660 CTGCAAGCTTGGCTATGAGGCTTCAAGGAGCTTCAACCGGCTTAAGAAAGATGAG 719
QY 725 CCTCAGCAGCTTCACTGACCTGACCTTGAAGGACATGCTTTCTGACCTGACCTT 783
DB 720 CCTCAGCAGCTTCACTGACCTTGAAGGACATGCTTTCTGACCTGACCTT 778

RESULT 10
ABK11647
ID ABK11647 standard; cDNA; 797 BP.
XX
XX ABK11647;
AC
XX
XX 05-JUN-2002 (first entry)
DT
XX
XX Human cDNA encoding novel neurotrophic factor NNT1.
DE
XX
XX Human; ss; gene; NNT1; neurotrophic factor; IGF-related disease;
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW vascular stenosis; rheumatoid arthritis; psoriatic arthritis;
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.

OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH 90..767
FT /*tag= a
FT /product= "NNT1"
XX
XX MO200215977-A2.
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US25906.
PF
XX
XX 18-AUG-2000; 2000US-226436P.
PR
XX 16-AUG-2001; 2001US-0931704.
PR
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Senaldi G;
PI
XX
XX MPI; 2002-280867/32.
DR
XX P-PSDB; AAU78176.
DR
XX
XX Treating Immunoglobulin E-related disease, modulating IGE levels in a
PT patient, preventing IGF-related disease and treating allergic diseases,
PT involves administering NNT-1 inhibitor to a patient
XX
XX
XX Claim 2; Fig 1; 63pp; English.

XX The invention relates to treating Immunoglobulin E (IGE)-related disease,
XX modulating IGE levels in a patient, preventing an IGF-related disease,
XX and treating allergic diseases, comprising administering a
XX therapeutically effective amount of novel neurotrophic factor (NNT)-1
XX inhibitor to a patient. Also included are a method of diagnosing an
XX IGE-related disease or susceptibility to an IGF-related disease, by
XX determining the presence or amount of expression of an NNT1 polypeptide

QY 662 GAGCTGACAGCTGCTATGCGCTTACGCCAGACTTCAACCGGCTTAAAGAGATG 721
DB 699 GAGCTGACAGCTGCTATGCGCTTACGCCAGACTTCAACCGGCTTAAAGAGATG 758
QY 722 GAGCTGACAGCTGCTATGCGCTTACGCCAGACTTCAACCGGCTTAAAGAGATG 781
DB 759 GAGCTGACAGCTGCTATGCGCTTACGCCAGACTTCAACCGGCTTAAAGAGATG 818
QY 782 CT 783
DB 819 TT 820
RESULT 7
AAV47510
ID AAV47510 standard; cDNA; 797 BP.
AC AAV47510;
XX
XX
XX 09-NOV-1998 (first entry)
DT
XX
XX Human neurotrophic factor NNT-1 cDNA.
DE
XX NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW peripheral neuropathy; dystrophy; neural retina degeneration;
KW common variable immunodeficiency; CVID; selective IgA deficiency;
KW hypogammaglobulinemia; X-linked agammaglobulinemia; antiseptic;
KW therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 90..767
FT sig_peptide 90..170
FT mat_peptide 171..764
FT /*tag= a
FT /*tag= b
FT /*tag= c
XX
XX W09833922-A1.
XX
XX 06-AUG-1998.
XX
XX 02-FEB-1998; 98MO-US02363.
XX
XX 30-JAN-1998; 98US-0016534.
XX 03-FEB-1997; 97US-0792019.
XX
XX (AMGE-) AMGEN INC.
XX
XX Chang M, Elliot GS, Sarmiento U, Senaldi G;
PI WPI; 1998-437475/37.
XX P-PSDB; AAW29715.
XX
XX Newly isolated nucleic acid encoding human or murine neurotrophic
PT factor NNT-1 - useful for treatment of neurological and
PT immunological diseases or inflammation, also as vaccine adjuvant
XX
XX
XX Claim 3; Fig 1; 120p; English.
XX
XX This newly isolated human cDNA sequence (deposited at ATCC 98295)
CC codes for a novel neurotrophic factor, designated NNT-1 (see
CC AAW29715), that is a growth factor for neurons and for B or T cells.
CC It was obtained from a T-cell lymphoma cDNA library by expressed
CC sequence tag analysis on the basis of homology to CNTF. The
CC isolated NNT-1 cDNA was used as probe to isolate NNT-1 genomic
CC DNA (see AAV47511). Vectors containing the cDNA or genomic DNA and
CC host cells are provided for use in the production of NNT-1
CC polypeptides. These are used to treat: (i) neurological or

CC immunological diseases, specifically Alzheimer's, Parkinson's or
CC Huntington's disease; amyotrophic lateral sclerosis,
CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
CC degeneration of the neural retina, or conditions characterised by T
CC or B cell defects, e.g. common variable immunodeficiency (CVID),
CC selective IgA deficiency, hypogammaglobulinemia and X-linked
CC agammaglobulinemia (claimed), but many others disclosed; and (ii)
CC inflammation. NNT-1 is also able to boost immunoreactivity and
CC antibody production following vaccination, and, since it inhibits
CC tumour necrosis factor production, it may also be useful for
CC treating sepsis. NNT-1 nucleic acid fragments are also used as
CC hybridisation probes in diagnostic assays. In addition, cells that
CC have been engineered to express NNT-1 can be implanted, or nucleic
CC acids are delivered in gene therapy vectors.
XX
XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;
SQ
Query Match 81.7%; Score 669.4; DB 19; Length 797;
Best Local Similarity 92.0%; Pred. No. 1.9e-158;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
QY 5 ATTTAAGCTTCCCGGAGCGCGGCTCCGCTCCCACTCCGACGCTTGGAGAGAG 64
DB 1 ATTTAAGCTTCCCGGAGCGCGGCTCCGCTCCCACTCCGACGCTTGGAGAGAG 60
QY 65 CCG 124
DB 61 CCG 119
QY 125 ATGTTAGCTTGGCTTATGACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 184
DB 120 ATGTTAGCTTGGCTTATGACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 179
QY 185 ACAGAGATCCAGGCGCTGCGCTTCCATCCAGAAACCTATGACCTGACCTGCTG 244
DB 180 ACAGAGATCCAGGCGCTGCGCTTCCATCCAGAAACCTATGACCTGACCTGCTG 239
QY 245 GAGCATCACTCCGAGGCTTATGCTGAGGACCTTACCTGAGGCGCGCGCTTCAAC 304
DB 240 GAGCATCACTCCGAGGCTTATGCTGAGGACCTTACCTGAGGCGCGCGCTTCAAC 299
QY 305 GAGCTGACTTCAATCTCTCTGACCTGCGGCGCGAGAACTGCGCGCGCGCGCGTCAAC 364
DB 300 GAGCTGACTTCAATCTCTCTGACCTGCGGCGCGAGAACTGCGCGCGCGCGCGTCAAC 359
QY 365 TTGGAAGTGTGCGGAGGCTTCAATGACGAGCTGCGCTGACCTGAGAGCGGTAC 424
DB 360 TTGGAAGTGTGCGGAGGCTTCAATGACGAGCTGCGCTGACCTGAGAGCGGTAC 419
QY 425 AGTCACTCTGCTGTATCTGCTGAGGCTTCAACCTGAGGCGCGCGCGCGCGTCAAC 484
DB 420 AGTCACTCTGCTGTATCTGCTGAGGCTTCAACCTGAGGCGCGCGCGCGCGTCAAC 479
QY 485 GGTACCTGCGGCACTTCTGTATCTGACGCTTCAAGGCGCTGCGGCGAGATGCGAGTGTG 544
DB 480 GGTACCTGCGGCACTTCTGTATCTGACGCTTCAAGGCGCTGCGGCGAGATGCGAGTGTG 539
QY 545 ATGCGAGGCTTGTGCTGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 604
DB 540 ATGCGAGGCTTGTGCTGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 599
QY 605 CCGTGGCG 664
DB 600 CCGTGGCG 659
QY 665 CTGCGAGACTGCTGCTATGCGCTTCAAGGAGCTTCAACCGGCTTAAAGAGATGCGAG 724
DB 660 CTGCGAGACTGCTGCTATGCGCTTCAAGGAGCTTCAACCGGCTTAAAGAGATGCGAG 719
QY 725 CTTGAGAGGCTTCAAGTACCTGCACTTGGAGGCACTGCTTGTGACCTTGAACCT 783
DB 720 CTTGAGAGGCTTCAAGTACCTGCACTTGGAGGCACTGCTTGTGACCTTGAACCT 778

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Oy 362 AACTGGAAGTGTGGCGAAGCCTCAATGACAGAGCTGCGGCTGAGCCAGAACATGAGCG 421
Db 441 GACTTGGAGTGTGGCGAAGCCTCAATGACAGAGCTGCGGCTGAGCCAGAACATGAGCG 500
Oy 422 TACAGTCACTCTGTGTGTTACTTGGCGCTCAACCGTCAAGCTGCGCAGCTGAATTC 481
Db 501 TACAGCCACCTTCTGTGTGTTACTTGGCGCTCAACCGTCAAGCTGCGCAGCTGAATTC 560
Oy 482 CGAGCTAGCTGCGCGCCCACTTGTGTAACAGAGCTGCGGCGCTGCGGCGAGCTGAGCT 541
Db 561 CGCGCAGCTGCGCGCCCACTTGTGTAACAGAGCTGCGGCGCTGCGGCGAGCTGAGCT 620
Oy 542 GTCATGCGAGCTGCGCTGAGTACCACTGCGCGCGCTGCGGCGAGCTGAGCTGAGCT 601
Db 621 GTCATGCGAGCTGCGCTGAGTACCACTGCGCGCGCTGCGGCGAGCTGAGCTGAGCT 680
Oy 602 GCCCTGCGCGCTGCGCGCGCGCTGCGGCGAGCTGAGCTGAGCTGAGCTGAGCT 661
Db 681 ACTCTGCGCGCTGCGCGCGCGCTGCGGCGAGCTGAGCTGAGCTGAGCTGAGCT 740
Oy 662 GAGCTGCGAGCTGCGCTGAGTACCACTGCGCGCGCTGCGGCGAGCTGAGCTGAGCT 721
Db 741 GAGCTGCGAGCTGCGCTGAGTACCACTGCGCGCGCTGCGGCGAGCTGAGCTGAGCT 800
Oy 722 CAGCTGCGAGCTGCGCTGAGTACCACTGCGCGCGCTGCGGCGAGCTGAGCTGAGCT 781
Db 801 CAGCTGCGAGCTGCGCTGAGTACCACTGCGCGCGCTGCGGCGAGCTGAGCTGAGCT 860
Oy 782 CT 783
Db 861 TT 862

```

RESULT 6

AAAB8546
ID AAAB8546 standard; DNA; 1790 BP.

AAAB8546;

22-JAN-2001 (first entry)

Human Interleukin-B60 (IL-B60) gene.

Interleukin-B60; IL-B60; human; cytokine; chromosome 11;

cytokine-like factor-1; haematopoietic; inflammation;

antiinflammatory; autoimmune disease; therapy; ds.

OS Homo sapiens.

PH Key location/Qualifiers

FT CDS 162..809

FT sig_peptide 162..212

FT mat_peptide 213..806

FT /tag= a

FT /tag= b

FT /tag= c

PN WO200053631-A1.

PD 14-SBP-2000.

PF 09-MAR-2000; 2000WO-US06182.

PR 11-MAR-1999; 99US-0267901.

PA (SCHB) SCHERING CORP.

PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;

DR WPI; 2000-587426/55.

XX P-PSDB; AAB19686.

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,

```

PT polypeptides, and nucleic acids, useful in research, diagnosis and for
PT treating inflammatory and autoimmune disorders -
XX
XX
PS Claim 17, Page 15-16; 97pp; English.
CC The present sequence is that of DNA encoding human interleukin-B60
CC (IL-B60, see AAB19586), a novel, small soluble cytokine-like protein
CC of 198 amino acids that exhibits structural motifs characteristic
CC of a member of the long-chain cytokines, and which shows homology
CC to granulocyte colony stimulating factor and interleukin-6. IL-608
CC may have either stimulatory or inhibitory effects on haematopoietic
CC cells, including e.g. lymphoid cells, such as T-cells, B-cells,
CC natural killer cells, macrophages, dendritic cells, haematopoietic
CC progenitors, etc. Methods are provided for modulating the
CC physiology or development of a cell or tissue culture cells by
CC contacting the cell with an agonist or antagonist of IL-B60 or an
CC agonist of antagonist of a complex of mature IL-B60 and its
CC partner, cytokine-like factor-1 (CLF-1, see AAB19588). The
CC IL-B60/CLF-1 cytokine serves as a key physiological factor in motor
CC neuron development and regeneration. IL-608, its agonists and
CC antagonists may be used to treat inflammatory or autoimmune
CC disorders and also for drug screening. The IL608 gene maps to
CC human chromosome 11.
SQ Sequence 1790 BP; 381 A; 560 C; 474 G; 375 T; 0 other;
Query Match 82.3%; Score 674; DB 21; Length 1790;
Best Local Similarity 92.2%; Pred. No. 1.6e-159;
Matches 721; Conservative 0; Mismatches 60; Indels 1; Gaps 1;
Oy 2 ATTATTAAAGCTGCGCGGAGCCGCGGCTGCGGCTGCGGCTGCGGCTGCGGAGAG 61
Db 40 ATTATTAAAGCTGCGCGGAGCCGCGGCTGCGGCTGCGGCTGCGGAGAG 99
Oy 62 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
Db 100 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 158
Oy 122 GGGATGTTAGCTGCGCTATGACAGGTGCTGCGGAGCTGCGGAGCTGCGGAGCT 181
Db 159 GGGATGTTAGCTGCGCTATGACAGGTGCTGCGGAGCTGCGGAGCTGCGGAGCT 218
Oy 182 CGCAGAGAGATTCAGGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
Db 219 CGCAGAGAGATTCAGGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 278
Oy 242 CTGAGAGATCACTCCGAGCTTATGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 301
Db 279 CTGAGAGATCACTCCGAGCTTATGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 338
Oy 302 AACGAGCTGACTTATCTCTCTGATGCGGCGCGGAGAACTTCCAGGCGCGCGCGCT 361
Db 339 AACGAGCTGACTTATCTCTCTGATGCGGCGCGGAGAACTTCCAGGCGCGCGCGCT 398
Oy 362 AACTGGAAGTGTGGCGAAGCCTCAATGACAGGCTGCGGCTGAGCCAGAACTATGAGCG 421
Db 399 GACTTGGAGTGTGGCGAAGCCTCAATGACAGGCTGCGGCTGAGCCAGAACTATGAGCG 458
Oy 422 TACAGTCACTCTGTGTGTTACTTGGCGCTCAACCGTCAAGCTGCGCAGCTGAATTC 481
Db 459 TACAGCCACCTTCTGTGTGTTACTTGGCGCTCAACCGTCAAGCTGCGCAGCTGAATTC 518
Oy 482 CGAGCTAGCTGCGCGCCCACTTGTGTAACAGAGCTGCGGCGCTGCGGCGAGCTGAGCT 541
Db 519 CGCGCAGCTGCGCGCCCACTTGTGTAACAGAGCTGCGGCGCTGCGGCGAGCTGAGCT 578
Oy 542 GTCATGCGAGCTGCGCTGAGTACCACTGCGCGCGCTGCGGCGAGCTGAGCTGAGCT 601
Db 579 GTCATGCGAGCTGCGCTGAGTACCACTGCGCGCGCTGCGGCGAGCTGAGCTGAGCT 638
Oy 602 GCCCTGCGCGCTGCGCGCGCGCTGCGGCGAGCTGAGCTGAGCTGAGCTGAGCT 661
Db 639 ACTCTGCGCGCTGCGCGCGCGCTGCGGCGAGCTGAGCTGAGCTGAGCTGAGCT 698

```


Oy		181	TGGCAGAGGAAATCCAGGCCCTGTGGCCCCCTCATTCACAAAAACCTATACCTCAACCGCTA	240		
Dd		181	TGGCAGAGGAAATCCAGGCCCTGTGGCCCCCTCATTCACAAAAACCTATACCTCAACCGCTA	240		
Oy		241	CCTGAGCAATCAACTCCGACGTTAGCTGGGAACCTAACACTACTGGGGCCCCCTT	300		
Dd		241	CCTGAGCAATCAACTCCGACGTTAGCTGGGAACCTAACACTACTGGGGCCCCCTT	300		
Oy		301	CAACGAGCCTGACTTTCAATCTCTTGACTGTGGGGGCAGAAAATTCTGCCCAGGGCACGGT	360		
Dd		301	CAACGAGCCTGACTTTCAATCTCTTGACTGTGGGGGCAGAAAATTCTGCCCAGGGCACGGT	360		
Oy		361	CAACTTGAAGTAGTGTGGCGAAGCCTCAATGACAGGCTGGGCTGACCAGAACTATGAGGC	420		
Dd		361	CAACTTGAAGTAGTGTGGCGAAGCCTCAATGACAGGCTGGGCTGACCAGAACTATGAGGC	420		
Oy		421	GTAACAATCACTCTCTGTGTTACTTGTGGCGCTCAACCCGTCAAGCTGCCACAGCTGAAT	480		
Dd		421	GTAACAATCACTCTCTGTGTTACTTGTGGCGCTCAACCCGTCAAGCTGCCACAGCTGAAT	480		
Oy		481	CCGACGTACCTCTGGCCCACTTCTGTACACAGCCTCCAGGGCTGTGGTGGCAGCAATTCAGG	540		
Dd		481	CCGACGTACCTCTGGCCCACTTCTGTACACAGCCTCCAGGGCTGTGGTGGCAGCAATTCAGG	540		
Oy		541	TGTCAATGGGAGGCTTGGGCTACCCACATGGCCCCAGCCTGTGGCCAGGAGCATGAGCAACCTG	600		
Dd		541	TGTCAATGGGAGGCTTGGGCTACCCACATGGCCCCAGCCTGTGGCCAGGAGCATGAGCAACCTG	600		
Oy		601	GGCCCCCTGGCCCTGTGCCACAGTGAATCTCTCCAGAAGATGATGACTTGTGGCTGTGAA	660		
Dd		601	GGCCCCCTGGCCCTGTGCCACAGTGAATCTCTCCAGAAGATGATGACTTGTGGCTGTGAA	660		
Oy		661	GGAGCTGCAGACCTGGGCTATGTGGCTTACGCCAAGACCTTCAACCGGCTTAAAGAAAGAT	720		
Dd		661	GGAGCTGCAGACCTGGGCTATGTGGCTTACGCCAAGACCTTCAACCGGCTTAAAGAAAGAT	720		
Oy		721	GGAGCCTCCAGGACGTTCACTGATCAACCCGTGACCTTGGAGGACACATGTTTTGACCTCTGAC	780		
Dd		721	GGAGCCTCCAGGACGTTCACTGATCAACCCGTGACCTTGGAGGACACATGTTTTGACCTCTGAC	780		
Oy		781	CCTTAACCCCAACCTCCAGGCGCCAGTCAAGCTGTGCTT	819		
Dd		781	CCTTAACCCCAACCTCCAGGCGCCAGTCAAGCTGTGCTT	819		
<hr/>						
RESULT 5						
AAH74484						
ID	AAH74484	standard; DNA; 881 BP.				
XX	AAH74484;					
AC						
XX						
DT	15-OCT-2001	(first entry)				
XX						
DE	Nucleotide sequence of a human NNT-1 protein.					
XX	NNT-1; CLE-1; SCNFAlpha; nervous system; neuron; nervous system;					
KM	neuro-muscular function; tumour; immune system; haematopoietic system;					
KW	reproductive system; liver; skeletal muscle; neurodegenerative disease;					
KV	amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;					
KW	muscular mass; paralysis; cancer; obesity; fertility; endometriosis;					
KM	blastocyst implantation; thrombosis; retinal disease;					
KX	retinal pigmentositis; ss.					
OS	Homo sapiens.					
XX						
FH	Key	Location/Qualifiers				
FT	CDS	174..851				
FT		/tag= a				
XX		/product= "NNT-1"				
PV	MO200155172-A2.					
XX						
DD	02-AUG-2001.					

Pf	XX		26-JAN-2001; 2001MO-FR00253.
Pr	XX		
Px	XX		27-JAN-2000; 2000FR-0001035.
Pr	XX		12-OCT-2000; 2000FR-0013089.
Pa	XX	(FABR)	FABRE MEDICAMENT SA PIERRE.
Pa	XX	(INRM)	INSERM INST NAT SANTE & RECH MEDICALE.
Pt	XX		
Pt	XX	Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H,	
Dr	XX	WPI; 2001-488773/53.	
Dr	XX	P-PsDB; AAG63543.	
Pt	XX		A complex comprising a NNT-1 protein and a CLF-1 and/or sCNTRALpha
Pt	XX		protein useful to treat neurodegenerative disease including Parkinson's
Pt	XX		and Huntington's, obesity and cancer
Pt	XX		-
Ps	XX		Disclosure; Page 57-58; 67pp; French.
Cc	XX		The present sequence encodes a human NNT-1 protein. The specification
Cc	XX		describes a complex comprising a NNT-1 protein and a CLF-1 and/or
Cc	XX		sCNTRALpha protein. The NNT-1/CLF-1 complex is used to modulate
Cc	XX		activity of the sCNTRALpha/gp130/LIFRbeta receptor complex, or to
Cc	XX		induce phosphorylation of the tyrosine of gp130 and LIFRbeta,
Cc	XX		particularly where cells expressing the receptor complex are in the
Cc	XX		central or peripheral nervous system, in neurons implicated in
Cc	XX		neuro-muscular function or in skeletal muscle. The complex or
Cc	XX		antibodies are also used to decrease the survival, growth or
Cc	XX		proliferation of tumour cells or to facilitate the proliferation and/or
Cc	XX		inhibit differentiation of cells stocks. The complex is also used to
Cc	XX		modulate activity of the gp130/LIFRbeta receptor or cells expressing
Cc	XX		this receptor, particularly those cells implicated in the immune,
Cc	XX		haematopoietic, nervous or reproductive system, the liver or skeletal
Cc	XX		muscle. Molecules of the invention may be used to prevent or treat
Cc	XX		neurodegenerative diseases including amyotrophic lateral sclerosis,
Cc	XX		Parkinson's and Huntington's disease, to repair or regenerate nervous
Cc	XX		or muscular tissue or to maintain muscular mass in paraplegia patients.
Cc	XX		They may also be used to treat cancer, obesity and associated diseases,
Cc	XX		and to improve fertility, particularly to avoid endometriosis and/or
Cc	XX		assist blastocyst implantation, thrombosis, or retinal disease,
Cc	XX		particular retinal pigmentositis.
Sq	XX		Sequence 881 BP; 158 A; 318 C; 246 G; 159 T; 0 other;
Query Match	82.3%;	Score 674;	DB 22; Length 881;
Best Local Similarity	92.2%;	Prod. No. 1.4e-159;	
Matches 721; Conservative	0;	Mismatches 60;	Indels 1; Gaps 1
Dy		2 ATATTAAGAAGCTTGCGGACCCGGCGGTGGCGCTCCGACTGCCGAGCCTTGGAGAG	61
Db		82 ATTATTAAAGCTTTGCGCGAACC GGAGCGTCCTGCCTCCCACTCCGCAAGCTTCGGAGAG	141
Dy		62 GAGCCGCGCCCGCGCGCGCCGCCGCCACCATGAGACTTCCGAGCAGGGAGCTCTGG	121
Db		142 GAGCGCGCACCCGGCGCGCGCGG -CCCCAGCCCAATGACCTCCGACGAGGGAGCTCTGG	200
Dy		122 GGAATGTTAGCTTGGCTATGACAGGTGTGTGGACCTTCCTGCAAGTGCACACTCTTAAT	181
Db		201 GGAATGTTAGGTGTCTGTGACAGGTGTCTTGGACCTTCCTGCAAGTGCACACTCTTAAT	260
Dy		182 CGCACAAGAGATCCAGAGCCCTGGGCCCCTCCATCCAGAAACCTTAGACTTCACCCGCTAC	241
Db		261 CGCACAAGGAGAACCCAGGGCCCTGGGCCCTTCATCCAGAAAACCTTAGACTTCACCCGCTAC	320
Dy		242 CTGAGAGCATCAACTCCGACGCTTAGCTGGAGCTTAACTGAATCTTGGGGCCGCCCTTTC	301
Db		321 CTGAGAGCACCAACTCCGAGACTTGGCTGGAGACTTATCTGAATCACTCTGGGCCGCCCTTTC	380
Dy		302 AACGAGCTGACTTCAATCTCTCTGACTGGGGGACGAAACTCTGACCAGGGCCACGGTC	361
Db		381 AACGAGCCAGACTTCAACCTCTCCCGCTGGGGGGACAGAGACTCTGCCAGGGCCCACTGTT	440

[illegible]

RESULT 4
ABK11649
ID ABK11649 standard; cDNA; 819 BP.

DT 05-JUN-2002 (first entry)
XX
DE Mouse CDNA encoding novel neurotrophic factor NNT1.
XX
KW Mouse; *ss*; gene; NNT1; neurotrophic factor; IgE-related disease;
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW vascular resensitization; rheumatoid arthritis; psoriatic arthritis;
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder
KW graft versus host disease; infertility; miscarriage; preterm labour.

OS	Mus sp.	Location/Qualifiers
XX		95..772
FH	Key	/*tag= a
FT	CDS	/product= "NN1"
FT		

WO200215977-A2

28-FEB-2002

17-AUG-2001; 2001WO-US25906.

18-AUG-2000; 2000US-226436P.

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צוה"מ, תשס"ח

Series

REF: 2002-260661132
P-PSDB: AA1178177

Treating Immunity

preventing IgE-related disease and treating allergic diseases,

Claim 2; Fig 4; 63pp; English.

CC The invention relates to treating Immunoglobulin E (IGE)-related disease,
CC modulating IGE levels in a patient, preventing an IGE-related disease,
CC and treating allergic diseases, comprising administering a
CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
CC inhibitor to a patient. Also included are a method of diagnosing an
CC IGE-related disease or susceptibility to an IGE-related disease, by
CC determining the presence or amount of expression of an NNT1 polypeptide
CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
CC occurring variant, and diagnosing an IGE-related disease or
CC susceptibility of an IGE-related disease based on the presence or amount
CC of expression of the polypeptide and a pharmaceutical composition for use
CC in treating IGE-related disease, comprising the NNT1 inhibitor.
CC The NNT1 inhibitor is useful for preventing and treating IGE-related
CC disease, modulating IGE levels, and treating allergic diseases e.g.,
CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,
CC pollinosis, asthma, immune diseases and disorders, diseases involving
CC abnormal cell proliferation including cancer, arteriosclerosis and
CC vascular stenosis, diseases and conditions relating to dysfunction of
CC immune system including rheumatoid arthritis, psoriatic arthritis,
CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,
CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
CC bowel disease, transplant rejection, and graft versus host disease, and
CC reproductive diseases and disorders including infertility, miscarriage,
CC preterm labour and delivery, and endometriosis. The present sequence
CC encodes mouse NNT1.

SQ Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;

Query Match	Score	DB	Length
100.0%	819	24	819

```
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	TATATATTAAGCTTCGCCGGAGCCGGGTGCCCTCCACTCCGCAACCTCTGGAGA	60
Db	1	TATATATTAAGCTTCGCCGGAGCCGGGTGCCCTCCACTCCGCAACCTCTGGAGA	60
Qy	61	GGAGCCGGCCCGCGCGCCCGGCCCCAGGCCCAATGGACTCCGAGCAGGGGACTCGTG	120
Db	61	GGAGCCGGCCCGCGCGCCCGGCCCCAGGCCCAATGGACTCCGAGCAGGGGACTCGTG	120
Qy	121	GGGGATGTTAGCTTCCTATGACAGGATGTGTGGACCTCCCTGACAGTCCAGACTCTTAA	180
Db	121	GGGGATGTTAGCTTCCTATGACAGGATGTGTGGACCTCCCTGACAGTCCAGACTCTTAA	180

CC The present sequence encodes a murine neurotrophic factor, designated
CC NNT-1, which is capable of stimulating growth of motor or sympathetic
CC neurons. The NNT-1 protein is useful in the treatment of neurological
CC diseases characterized by the degeneration and death of particular
CC classes of neurons. These diseases specifically include Parkinson's
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
CC stroke and various degenerative disorders affecting vision.

XX Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;

Query Match 100.0%; Score 819; DB 19; Length 819;

Best Local Similarity 100.0%; Pred. No. 5.1e-196;

Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TATTATTAAAGCTTGCCTGAGAGCGGCTGCGCTCCCACTCCGCGAGCTTGGAGAA 60
DB 1 TATTATTAAAGCTTGCCTGAGAGCGGCTGCGCTCCCACTCCGCGAGCTTGGAGAA 60
OY 61 GGAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 61 GGAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
OY 121 GGGGATGTAGCTTGCCTATGACAGGCTGCTGTGGCACTTCCCTGCACTGCTTAA 180
DB 121 GGGGATGTAGCTTGCCTATGACAGGCTGCTGTGGCACTTCCCTGCACTGCTTAA 180
OY 181 TGGCAGAGAGATCCAGAGCGCTGCGCTCCATCCAGAAACCTATAGACTACCGGCTA 240
DB 181 TGGCAGAGAGATCCAGAGCGCTGCGCTCCATCCAGAAACCTATAGACTACCGGCTA 240
OY 241 CCTGAGATCAATCCGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 300
DB 241 CCTGAGATCAATCCGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 300
OY 301 CAACGAGCTGACTTAATCTCTCTGACTGCTGGGAGGAACTCTGCGCGCGCGCT 360
DB 301 CAACGAGCTGACTTAATCTCTCTGACTGCTGGGAGGAACTCTGCGCGCGCGCT 360
OY 361 CAACCTGGAAGTGTGGCGAAGCTCAATGACAGGCTGCGCGCTGACCCAGAACTATGAGGC 420
DB 361 CAACCTGGAAGTGTGGCGAAGCTCAATGACAGGCTGCGCGCTGACCCAGAACTATGAGGC 420
OY 421 GTACAGTCACTCTGTGTACTTGTGCTGAGCTCAACCGTCAAGGCTGCGCGAGCTGAACT 480
DB 421 GTACAGTCACTCTGTGTACTTGTGCTGAGCTCAACCGTCAAGGCTGCGCGAGCTGAACT 480
OY 481 CCGAGCTGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
DB 481 CCGAGCTGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
OY 541 TGTCAATGGAGAGCTTGGCTACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
DB 541 TGTCAATGGAGAGCTTGGCTACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
OY 601 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 601 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
OY 661 GGAAGCTGACAGCTTGTGCTGAGCTTCCCTCAAGAGATGATGATCTTGTGCTGTA 720
DB 661 GGAAGCTGACAGCTTGTGCTGAGCTTCCCTCAAGAGATGATGATCTTGTGCTGTA 720
OY 721 GGAAGCTTCCAGAGCTTGTGCTGAGCTTCCCTCAAGAGATGATGATCTTGTGCTGTA 780
DB 721 GGAAGCTTCCAGAGCTTGTGCTGAGCTTCCCTCAAGAGATGATGATCTTGTGCTGTA 780
OY 781 CCTTAACCCCACTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 819
DB 781 CCTTAACCCCACTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 819
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RESULT 3
AAA39483

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ID AAA39483 standard; cDNA; 819 BP.
XX
AC AAA39483;
XX
DT 24-AUG-2000 (first entry)
XX
DE Murine NNT-1 cDNA.
XX
KW NNT-1; neurotrophic factor; neuroprotective; treatment;
KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine;
KW Huntington's disease; peripheral neuropathy; neural retina degeneration;
KW retinopathy; immune disorder; hematopoietic disorder; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 95..772
FT /tag= a
FT /product= "NNT-1"
XX
XX US6054294-A.
XX
XX 25-APR-2000.
XX
XX 12-DEC-1997; 97US-0988819.
XX
XX 03-FEB-1997; 97US-0792019.
XX
XX (AMGE-) AMGEN INC.
XX
XX Chang M;
XX
XX WPI; 2000-338492/29.
XX
XX P-PSDB; AAY87814.
XX
XX New nucleic acids encoding neurotrophic factors useful for stimulating
XX growth of motor or sympathetic neurons for treating neuron cell damage
XX
XX Claim 2a; Fig 4; 42pp; English.
XX
XX This invention describes a novel nucleic acid molecule (i) encoding a
XX novel neurotrophic factor (NNT-1) (ii) which has neurotrophic,
XX neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
XX ophthalmological activity. (I) is useful for producing NNT-1
XX polypeptides which are useful for treating patients in whom various
XX cells of the central, autonomic, or peripheral nervous system have
XX degenerated and/or have been damaged by congenital disease, trauma,
XX mechanical damage, surgery, stroke, ischemia, infection, metabolic
XX disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
XX proteins are used to treat diseases like Alzheimer's, Parkinson's,
XX amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
XX disease, peripheral neuropathy induced by diabetes or other metabolic
XX disorders, and/or dystrophies or degeneration of the neural retina such
XX as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
XX night blindness, progressive cone-rod degeneration, immune disorders and
XX hematopoietic disorders. (I) is effective in treating neurological
XX conditions and promotes neuron regeneration. Neural functions are
XX effectively restored in patients suffering from various neurological
XX disorders. This sequence encodes the murine NNT-1 protein described in
XX the method of the invention.
XX
XX Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;
XX
Query Match 100.0%; Score 819; DB 21; Length 819;
Best Local Similarity 100.0%; Pred. No. 5.1e-196;
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TATTATTAAAGCTTGCCTGAGAGCGGCTGCGCTCCCACTCCGCGAGCTTGGAGAA 60
DB 1 TATTATTAAAGCTTGCCTGAGAGCGGCTGCGCTCCCACTCCGCGAGCTTGGAGAA 60
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Search completed: February 9, 2004, 09:36:34
Job time : 381.326 secs

/ TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
/ FILE REFERENCE: 44921-5028-WO
/ CURRENT APPLICATION NUMBER: US/09/880,107.
/ CURRENT FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: US 60/211,379
/ PRIOR FILING DATE: 2000-06-14
/ PRIOR APPLICATION NUMBER: US 60/237,054
/ PRIOR FILING DATE: 2000-10-02
/ NUMBER OF SEQ ID NOS: 3950
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3440
/ LENGTH: 1578
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. US20020142981A1 U82108
US-09-880-107-3440

Query Match 5.2%; Score 42.4; DB 10; Length 1578;
Best Local Similarity 52.9%; Pred. No. 0.047;
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 512 CTCGAGGGCTCTGGGCGAGCTGTCAGGTGTCAGCGCTTGGCTACCGCTAGCCG 571
DB 377 CTCGCGCGGCGGCGAGCTGTACCGAGAGATGGCCGAGGGCTCCACCGCC 436
QY 572 CAGCCTTCCGAGGAGCTGAGCGCTGGGCGCCCTGGCCCTCCAGAGTACTTCC 631
DB 437 CAGGACCCCTGGAGCGGAGGCTGAGCTGGGCGACACACCGGAGCCGAGCTCCGAA 496
QY 632 CAGAGATGATGATCTTGTGCTGCTGAAGAGCTGAGAGCTGGCTATGCG 683
DB 497 GCGAAGAGATGTCTAGTGGGCGCTGAGGAGCTGCGCCCTCGGCTCTGCG 548

RESULT 15
US-10-108-260A-1682
/ Sequence 1682, Application US/10108260A
/ Publication No. US20040005560A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/10/108,260A
/ CURRENT FILING DATE: 2002-03-27
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1682
/ LENGTH: 2750
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-108-260A-1682

Query Match 5.0%; Score 40.8; DB 12; Length 2750;
Best Local Similarity 51.8%; Pred. No. 0.14;
Matches 116; Conservative 0; Mismatches 107; Indels 1; Gaps 1;

QY 19 GAGAGCGGCGCTCGCCCTCCACTCGCCAGCCTTGGAGAGAGCGCGCGCGCG 78
DB 1285 GAGAGAGTGAAGCTCCAGCGCCACACACGAGCCCTGTCTCCCCACCGCCCA 1344
QY 79 CCGGCGCGGCGGCGGCGGAGCTCGAGCGGAGCTGTGGGGAGTTAGTTGCGCT 138
DB 1345 ACTGCCCCCAACTCTCTGGGAGATCCCTCATGAGCGCGCTTTCTATGGGGTGAAGCA 1404
QY 139 ATGCAAGGTGCTGTGGCACTCTCGAGTGC-CAGCTTTATGSCACAGAGATCCAG 197
DB 1405 GGGCGAGGGGTGGGGGCGCGCGGCGAGTGAACACTTCAACGCTAACCGCGCGG 1464
QY 198 GCGCTGGCCCTCTCCATCCAGAAACCTATGACTCACCGGCTAC 241
DB 1465 TCTGTGCCCCCTGCGACCCGAGCCCACTCTCCAGCGAC 1508

NAME/KEY: Site
LOCATION: (306)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (360)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (371)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (377)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (383)
OTHER INFORMATION: n equals any nucleotide
US-10-212-793-7

Query Match
Best Local Similarity 6.3%; Score 52; DB 15; Length 396;
Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 716 AAGATGACCTTCAGACAGCTTCAGTACCTGAGGACAGTGGTTCTGACCT 775
DB 4 ACGAGCAGCTTCAGACAGCTTCAGTACCTGAGGACAGTGGTTCTGACCT 63
QY 776 CTGACCT 783
DB 64 CTGACCT 71

RESULT 12
US-10-156-761-1403/c
Sequence 1403, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1403
LENGTH: 951
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(951)
US-10-156-761-1403

Query Match
Best Local Similarity 5.6%; Score 46; DB 15; Length 951;
Matches 103; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 430 CCTCTGTGTTACTTGGCGGCTTCAACCTGACAGCTGCAAGTGAAGTCCGACGTG 489
DB 562 CCTCAGCGCTGAACAGGCGGAGCGTCCGCGGCCCAAGCGTGTGATCAAGGTCA 503
QY 490 CCTGCCCCACTTGTATCAGAGCTTCAGGCGCTGCTGGCAGCATTTGACGTATGAC 549

DB 502 TCTCGCCAGCTTCGCCAGTCCGACGAGGTGCGGTCCGTACTGTCTCGCGGTCA 443
QY 550 GACGTTGGCTACCCATGCGCCAGCTTCTGACAGGACTGAGGCGGAGCTGGGCGCTGG 609
DB 442 GAGCATGTAGCGCTTCTGCGCCCATCAGCGGAGCGGTGAGGAGCTCCGCTCCCGC 383
QY 610 CCTGCCCCAGTGAATT 627
DB 382 ACCTACCTGCGCGCTTT 365

RESULT 13
US-10-156-761-1
Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match
Best Local Similarity 5.6%; Score 46; DB 15; Length 9025608;
Matches 103; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 430 CCTCTGTGTTACTTGGCGGCTTCAACCTGACAGCTGCAAGTGAAGTCCGACGTG 489
DB 1746625 CCTCAGCGCTGAACAGGCGGAGCGTCCGCGGCCCAAGCGTGTGATCAAGGTCA 1746684
QY 490 CCTGCCCCACTTGTATCAGAGCTTCAGGCGCTGCTGGCAGCATTTGACGTATGAC 549
DB 1746685 TCTGCCCCAGCTTCGCCAGTCCGAGCGAGGTGCGTCCGTGCTGTGCGGTCA 1746744
QY 550 GACGTTGGCTACCCATGCGCCAGCTTCTGACAGGACTGAGGCGGAGCTGGGCGCTGG 609
DB 1746745 GAGCATGTAGCGCTTCTGCGCCCATCAGCGGAGCGGTGAGGAGCTCCGCTCCCGC 1746804
QY 610 CCTGCCCCAGTGAATT 627
DB 1746805 ACCTACCTGCGCGCTTT 365

RESULT 14
US-09-880-107-3440
Sequence 3440, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darcil T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.

US-10-027-632-134702

Query Match 19.3% Score 158; DB 13; Length 809;
Best Local Similarity 88.5%; Pred. No. 7.9e-35;
Matches 170; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

QY 100 CCTCGAGAGGAGGACTCGTGGGGGATGTTAGCTTGCCTTATCAGCGTGTGTGACACT 159
DB 46 CTGCGCCACAGGGAGCTCGTGGGGATGTTAGCGTGTGTGACAGTGTCTGTGGACACT 105
QY 160 CCTCGAGTGGCAGCTCTTAATGCGACAGAGATCCAGGCTGTGGCCCTTCATCCAGAA 219
DB 106 CCTCGAGTGGCAGCTCTTAATGCGACAGAGATCCAGGCTGTGGCCCTTCATCCAGAA 165
QY 220 AACCTATGACTCACCCTGCTTACCTGAGCATCACTCGCAGCTTAGCTGGAGCTTACT 279
DB 166 AACCTATGACTCACCCTGCTTACCTGAGCATCACTCGCAGCTTAGCTGGAGCTTACT 225
QY 280 GAATACCTGGG 291
DB 226 GAGTATCCAGCG 237

RESULT 9
US-10-027-632-134702
; Sequence 134702, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; PRIOR FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 134702

; LENGTH: 809

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-134702

Query Match 19.3% Score 158; DB 14; Length 809;
Best Local Similarity 88.5%; Pred. No. 7.9e-35;

Matches 170; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

QY 100 CCTCGAGAGGAGGACTCGTGGGGGATGTTAGCTTGCCTTATCAGCGTGTGTGACACT 159
DB 46 CTGCGCCACAGGGAGCTCGTGGGGATGTTAGCGTGTGTGACAGTGTCTGTGGACACT 105
QY 160 CCTCGAGTGGCAGCTCTTAATGCGACAGAGATCCAGGCTGTGGCCCTTCATCCAGAA 219
DB 106 CCTCGAGTGGCAGCTCTTAATGCGACAGAGATCCAGGCTGTGGCCCTTCATCCAGAA 165
QY 220 AACCTATGACTCACCCTGCTTACCTGAGCATCACTCGCAGCTTAGCTGGAGCTTACT 279
DB 166 AACCTATGACTCACCCTGCTTACCTGAGCATCACTCGCAGCTTAGCTGGAGCTTACT 225
QY 280 GAATACCTGGG 291
DB 226 GAGTATCCAGCG 237

DB 226 GAGTATCCAGCG 237

RESULT 10
US-09-908-975-29446
; Sequence 29446, Application US/09908975

; Publication No. US20030165843A1

; GENERAL INFORMATION:

; APPLICANT: SHOSHAN, Avi

; APPLICANT: WASSERMAN, Alon

; APPLICANT: MINTZ, Eli

; APPLICANT: FAIGLER, Simchon

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC

; FILE REFERENCE: 36688-0005

; CURRENT APPLICATION NUMBER: US/09/908,975

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/287,724

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/221,607

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 32337

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 29446

; LENGTH: 65

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-908-975-29446

Query Match 7.9% Score 65; DB 13; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 CTGAAGAGCTGCGAGCTGCTATGCGCTTACGCAAGAGCTTCAACCGGCTTAAGAAG 715
DB 1 CTGAAGAGCTGCGAGCTGCTATGCGCTTACGCAAGAGCTTCAACCGGCTTAAGAAG 60
QY 716 AAGAT 720
DB 61 AAGAT 65

RESULT 11
US-10-212-793-7

; Sequence 7, Application US/10212793

; Publication No. US20030087395A1

; GENERAL INFORMATION:

; APPLICANT: Shi et al.

; TITLE OF INVENTION: Cardiotrophin-Like Cytokine

; FILE REFERENCE: PE385D1C1

; CURRENT APPLICATION NUMBER: US/10/212,793

; PRIOR FILING DATE: 2002-08-07

; PRIOR APPLICATION NUMBER: US 09/438,299

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: US 09/106,182

; PRIOR FILING DATE: 1998-06-29

; PRIOR APPLICATION NUMBER: US 60/051,311

; NUMBER OF SEQ ID NOS: 24

; SEQ ID NO 7

; LENGTH: 396

; TYPE: DNA

; ORGANISM: homo sapiens

; FEATURE:

; NAME/KEY: Site

; LOCATION: (199)

; OTHER INFORMATION: n equals any nucleotide

; NAME/KEY: Site

; LOCATION: (293)

; OTHER INFORMATION: n equals any nucleotide

; FEATURE:

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 6462
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005849.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; US-09-864-761-6462

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Query Match Best Local Similarity 36.5%; Score 299.2; DB 9; Length 492;

Matches 319; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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QY 432 TCTGTGTTACTTCTGCGCTTCAACCGTCAGGCTGCGACGCTGACCTCCGACGTAGCC 491
DB 492 TTCTGTGTTACTTCTGCGCTTCAACCGTCAGGCTGCGACGCTGACCTCCGACGTAGCC 433
QY 492 TGGCCCACTTCTGTATCAACGCTTCCAGGCTGCTGCGGAGCATTTGCAAGGTGTCATGCGCA 551
DB 432 TGGCCCACTTCTGTATCAACGCTTCCAGGCTGCTGCGGAGCATTTGCAAGGTGTCATGCGCA 373
QY 552 CGCTTGGCTTACCACTGCGGCTTCCAGGCTTCCAGGCTGCGGAGCATTTGCAAGGTGTCATGCGCA 611
DB 372 TCTGTGCTTACCACTGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT 313
QY 612 CTGCCCACTGACCTTCTTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
DB 312 CTGCCCACTGACCTTCTTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 253
QY 672 CCGGTATGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 731
DB 252 CCGGTATGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 193
QY 732 CAGCTTCACTGACCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 783
DB 192 CAGCTTCACTGACCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 141

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RESULT 7
US-09-765-231A-75
Sequence 75, Application US/09765231A
Patent No. US20020119452A1
GENERAL INFORMATION:

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; APPLICANT: Seale/Monsanto
; APPLICANT: Phippar, Deborah
; APPLICANT: Vasanthakumar, Geetha
; APPLICANT: Dotson, Stanton
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
; FILE REFERENCE: SO-3221 PR
; CURRENT APPLICATION NUMBER: US/09/765,231A
; NUMBER OF SEQ ID NOS: 82
; SEQ ID NO 75
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-765-231A-75

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Query Match Best Local Similarity 28.8%; Score 236; DB 10; Length 283;

Matches 267; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

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QY 41 CTCGCCACCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 100
DB 1 CTCGCCACCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 59
QY 101 CTCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159
DB 60 CTCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 119
QY 160 CCTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 219
DB 120 CCTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179
QY 220 AACCTATGACCTTCAACCGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 279
DB 180 AACCTATGACCTTCAACCGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 239
QY 280 GAACCTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323
DB 240 GAACCTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 283

```

RESULT 8

US-10-027-632-134702
Sequence 134702, Application US/10027632
Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 134702

TYPE: DNA

ORGANISM: Human


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QY 1 TATTATTAAGCTTGGCCGAGCCGCGCTCCCTCCCACTCCGCGACGCTCTGGAGAG 60
DB 1 TATTATTAAGCTTGGCCGAGCCGCGCTCCCTCCCACTCCGCGACGCTCTGGAGAG 60
QY 61 GGAGCCGCGCCCGCCGCGCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 120
DB 61 GGAGCCGCGCCCGCCGCGCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 120
QY 121 GGGGATGTTAGCTTGGCTTGAAGGCTGTGGCACTCTCGACAGTGGCACTCTTAA 180
DB 121 GGGGATGTTAGCTTGGCTTGAAGGCTGTGGCACTCTCGACAGTGGCACTCTTAA 180
QY 181 TGGCAGCAGAGATCCAGGCGCTGGCCCTCCATCCAGAAAACCTTATGACCTACCCGCTA 240
DB 181 TGGCAGCAGAGATCCAGGCGCTGGCCCTCCATCCAGAAAACCTTATGACCTACCCGCTA 240
QY 241 CTTGAGAGCTCAACTCCGAGCTTAGCTGGAGCTTACCTGAACCTAGCGGGCCCTTT 300
DB 241 CTTGAGAGCTCAACTCCGAGCTTAGCTGGAGCTTACCTGAACCTAGCGGGCCCTTT 300
QY 301 CAACGAGCTGACTTCAATCTCTCTGACTGGGGGCAAAAACCTTGGCCCGCCAGCGT 360
DB 301 CAACGAGCTGACTTCAATCTCTCTGACTGGGGGCAAAAACCTTGGCCCGCCAGCGT 360
QY 361 CAACCTTGAAGTGTGGGAGGCTCAATGACAGGCTGGCGGCTGACCCAGAACTATGAGGC 420
DB 361 CAACCTTGAAGTGTGGGAGGCTCAATGACAGGCTGGCGGCTGACCCAGAACTATGAGGC 420
QY 421 GTACAGTCACTCTGTGTTAATTGCTGGGCTTCAACCGTGAAGGCTGACAGCTGAAC 480
DB 421 GTACAGTCACTCTGTGTTAATTGCTGGGCTTCAACCGTGAAGGCTGACAGCTGAAC 480
QY 481 CCGAGCTGAGCTTGGCCCACTTCTGTAACAGCTTCCAGGGCTGTGGGAGCATTTGACG 540
DB 481 CCGAGCTGAGCTTGGCCCACTTCTGTAACAGCTTCCAGGGCTGTGGGAGCATTTGACG 540
QY 541 TGTCAATGGGAGCTTGGCTTACCACTGCGCCAGGCTCTGCGCAAGGAGCTGACCGACCTG 600
DB 541 TGTCAATGGGAGCTTGGCTTACCACTGCGCCAGGCTCTGCGCAAGGAGCTGACCGACCTG 600
QY 601 GGGCCCTGGCCCTGCGCCACAGTACTTCTCCAGAAATGATGACTTGTGCTCTGA 660
DB 601 GGGCCCTGGCCCTGCGCCACAGTACTTCTCCAGAAATGATGACTTGTGCTCTGA 660
QY 661 GAGAGCTGAGAGCTTGGCTTATGGCTTCAAGCAAGACTTCAACCGGCTTAAAGAAAGAT 720
DB 661 GAGAGCTGAGAGCTTGGCTTATGGCTTCAAGCAAGACTTCAACCGGCTTAAAGAAAGAT 720
QY 721 GAGAGCTTCAAGAGCTTCAAGTCACTTGGAGCATTTGTTCTGACTCTGAC 780
DB 721 GAGAGCTTCAAGAGCTTCAAGTCACTTGGAGCATTTGTTCTGACTCTGAC 780
QY 781 CCTTAACCCCAACCTTCCAGGCGCCAGTCAAGCTGTGCTT 819
DB 781 CCTTAACCCCAACCTTCCAGGCGCCAGTCAAGCTGTGCTT 819
RESULT 2
US-09-931-704-1
; Sequence 1, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using N
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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LENGTH: 797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (90)..(764)
OTHER INFORMATION:
NAME/KEY: mat peptide
LOCATION: (171)..()
OTHER INFORMATION: Met at -27
US-09-931-704-1

Query Match 81.7%; Score 669.4; DB 9; Length 797;
Best Local Similarity 92.0%; Pred. No. 1.2e-179;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 5 ATTAAGCTTGGCCGAGCCGCGCTCCCTCCCACTCCGCGACGCTCTGGAGAGAG 64
DB 1 ATTAAGCTTGGCCGAGCCGCGCTCCCTCCCACTCCGCGACGCTCTGGAGAGAG 60
QY 65 CCGGCGCCGCGCCGCGCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 124
DB 61 CCGGCGCCGCGCCGCGCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 119
QY 125 ATGTTAGCTTGGCTTGAAGGCTGTGGCACTCTCGACAGTGGCACTTAAATGC 184
DB 120 ATGTTAGCTTGGCTTGAAGGCTGTGGCACTCTCGACAGTGGCACTTAAATGC 179
QY 185 ACAGAGATCCAGGCGCCGCGCTCCATCCAGAAAACCTTATGACCTACCCGCTACCTG 244
DB 180 ACAGAGATCCAGGCGCCGCGCTCCATCCAGAAAACCTTATGACCTACCCGCTACCTG 239
QY 245 GAGCATCACTCCGAGCTTAGCTGGAGCTTAACTTAACTTGGGGCCCTTTCAAC 304
DB 240 GAGCATCACTCCGAGCTTAGCTGGAGCTTAACTTAACTTGGGGCCCTTTCAAC 299
QY 305 GAGCTGACTTCAATCTCTCTGACTGGGGGCAAAAACCTTGGCCCGCCAGCGTCAAC 364
DB 300 GAGCTGACTTCAATCTCTCTGACTGGGGGCAAAAACCTTGGCCCGCCAGCGTCAAC 359
QY 365 TTGGAAGTGTGGGAGGCTCAATGACAGGCTGGCGGCTGACCCAGAACTATGAGCGTAC 424
DB 360 TTGGAAGTGTGGGAGGCTCAATGACAGGCTGGCGGCTGACCCAGAACTATGAGCGTAC 419
QY 425 AGTCACTCTGTGTTAATTGCTGGGCTTCAACCGTCAAGGCTGCAAGCTGAACCTCGA 484
DB 420 AGTCACTCTGTGTTAATTGCTGGGCTTCAACCGTCAAGGCTGCAAGCTGAGCTGCGC 479
QY 485 GGTAGCTTGGCCCACTTCTGTAACAGGCTTCCAGGGGCTGTGGGAGCATTTGAGGTGC 544
DB 480 GGTAGCTTGGCCCACTTCTGTAACAGGCTTCCAGGGGCTGTGGGAGCATTTGAGGTGC 539
QY 545 ATGGCAGGCTTGGCTTACCTCCAGGCTTGTGCGAGGAGCATGAGCGCTGGGCC 604
DB 540 ATGGCAGGCTTGGCTTACCTCCAGGCTTGTGCGAGGAGCATGAGCGCTGGGCC 599
QY 605 CTTGGCCCTTCCCAAGTACTTCTTCCAGAAATGATGACTTGTGCTCTTAAAGAG 664
DB 600 CTTGGCCCTTCCCAAGTACTTCTTCCAGAAATGATGACTTGTGCTCTTAAAGAG 659
QY 665 CTGCAAGCTTGGCTTATGGCTTCAAGCAAGACTTCAACCGGCTTAAAGAAATGAG 724
DB 660 CTGCAAGCTTGGCTTATGGCTTCAAGCAAGACTTCAACCGGCTTAAAGAAATGAG 719
QY 725 CTTCCAGAGCTTCAAGTACCTTCACTTGGAGGCACTGTTCTGACTCTGACCT 783
DB 720 CTTCCAGAGCTTCAAGTACCTTCACTTGGAGGCACTGTTCTGACTCTGACCT 778
RESULT 3
US-10-212-793-1
; Sequence 1, Application US/10212793
; Publication No. US20030087395A1
```



```

APPLICANT: Seedorf, Klaus
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF TKA-1 RELATED
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,037
FILING DATE: June 13, 1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,167
FILING DATE: October 13, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 220/156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1642 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 97...1446
US-08-665-037-1

Query Match 5.2%; Score 42.4; DB 2; Length 1642;
Base Local Similarity 52.9%; P-adj. 0.057;
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0

512 CTCGAGGCGCTGCTGAGGAGCATTCGAGGCTGTCATGCGAGCGCTTGAGTACCACTGAGCC 571
|||||
379 CTCGCGCCGCGGCGAGCTGTAACCTGACCGAGAGATGCGCCAGAGAGGCTCCACCCGCC 438
|||||
572 GAGCCTTGCCAGGAGCTGAGCGAGCGCTGGGCGCCCTGCGCCACAGTGAATTCTTC 631
|||||
439 CACGACCCCTGGAGCCGAGCCAGCCAGCTGAGGACACACAGCGGCGACGAGCTCCGAAGCT 498
|||||
632 CAGAAAGATGATGACTTCTGCTGCTGGAAGAGAGCTGCAACCTGGCTATGGC 683
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499 GCGCAAGAGGAGATGCTCAGTGCGGCCCTTGAAGAGAGCTGCGCTCGCTGCGC 550
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RESULT 12

US-08-665-259-19/c

; Sequence 19, Application US/08665259

; Patent No. 6028173

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Burn, Timothy C.

; APPLICANT: Connors, Timothy D.

; APPLICANT: Dackowski, William R.

; APPLICANT: Van Raay, Terence J.

; APPLICANT: Klingner, Katherine W.

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESS: GENZYME CORPORATION

; STREET: One Mountain Road

; CITY: Framingham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 01701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/665,259

; FILING DATE: 17-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Dugan, Deborah A.

; REGISTRATION NUMBER: 37,315

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 872-8400

; TELEFAX: (508) 872-5415

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6803 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-665-259-19

; US-08-665-259-19

Query Match 5.3%; Score 43.2; DB 3; Length 6803;
Best Local Similarity 49.6%; Pred. No. 0.054;
Matches 111; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 24 CGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCGCG 83
DB 6708 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCG 6649
QY 84 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCGCG 143
DB 6648 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCG 6589
QY 144 CGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCGCG 203
DB 6588 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCG 6529
QY 204 GCGGCTTCATCCAGAAACTTATGACTTACCCGCTACTGAG 247
DB 6528 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCG 6485

RESULT 13

US-08-762-500-19/c

; Sequence 19, Application US/08762500

; Patent No. 6030806

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Burn, Timothy C.

; APPLICANT: Connors, Timothy D.

; APPLICANT: Dackowski, William R.

; APPLICANT: Van Raay, Terence J.

; APPLICANT: Klingner, Katherine W.

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

; NUMBER OF SEQUENCES: 83

; CORRESPONDENCE ADDRESS:

; ADDRESS: GENZYME CORPORATION

; STREET: One Mountain Road

; CITY: Framingham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 01701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/762,500

; FILING DATE: 09-DEC-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/665,259

; FILING DATE: 17-JUN-1996

; PRIOR APPLICATION DATA: PCT/US96/10469

; APPLICATION NUMBER: 17-JUN-1996

; FILING DATE: 17-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Dugan, Deborah A.

; REGISTRATION NUMBER: 37,315

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 872-8400

; TELEFAX: (508) 872-5415

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6803 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-762-500-19

; US-08-762-500-19

Query Match 5.3%; Score 43.2; DB 3; Length 6803;
Best Local Similarity 49.6%; Pred. No. 0.054;
Matches 111; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 24 CGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCGCG 83
DB 6708 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCG 6649
QY 84 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCGCG 143
DB 6648 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCG 6589
QY 144 CGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCGCG 203
DB 6588 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCGCG 6529
QY 204 GCGGCTTCATCCAGAAACTTATGACTTACCCGCTACTGAG 247
DB 6528 CCGGGGCTGGCCCTCCCACTCCGCGAGCTCTGTGGAGAGAGCCGCGCGCG 6485

RESULT 14

US-08-665-037-1

; Sequence 1, Application US/08665037

; Patent No. 5895813

; GENERAL INFORMATION:

RESULT 10
US-09-016-534-3
Sequence 3, Application US/09016534
Patent No. 6143874
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: ELLIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SEMALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 137_138 /Product = "INTERVENING UNSEQUENCED
OTHER INFORMATION: REGION OF >1KB"
US-09-016-534-3
Query Match 52.5%; Score 429.6; DB 3; Length 5087;
Best Local Similarity 90.4%; Pred. No. 2,8e-103;
Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 276 ACTGTAACCTCTGAGGAGCCCTTTCAAGAGCCTGACTTCAATCTCTGACTGAGG 335
DB 3363 AGCTGAACCTCTGAGGAGCCCTTTCAAGAGCCTGACTTCAATCTCTGAGG 3422
QY 336 CAGAACTCTGAGGAGCCCTTTCAAGAGCCTGACTTCAATCTCTGAGG 395
DB 3423 CAGAACTCTGAGGAGCCCTTTCAAGAGCCTGACTTCAATCTCTGAGG 3482
QY 396 TGGGCTGACCCAGAACTATGAGGCGTACAGTCACTCTGTGTTACTTGGGCTGCA 455
DB 3443 TGGGCTGACCCAGAACTATGAGGCGTACAGTCACTCTGTGTTACTTGGGCTGCA 3542
QY 456 ACCGTGAGCTGCCAGAGCTGAACTCCAGAGCTGAGCTGAGCCCACTTCTGTACAGGCTCC 515
DB 3543 ACCGTGAGCTGCCAGAGCTGAACTCCAGAGCTGAGCTGAGCCCACTTCTGTACAGGCTCC 3602
QY 516 AGGGCTGCTGGGCGAGATTGCAAGTGTATGAGGCGAGCCTTGGCTACCACTGCCCCAGC 575
DB 3603 AGGGCTGCTGGGCGAGATTGCAAGTGTATGAGGCGAGCCTTGGCTACCACTGCCCCAGC 3662

QY 576 CTGTCCAGGAGCTGAGCAGAGCCTGAGGAGCCCTGAGCCGACCAAGTACTTCTCCAGA 635
DB 3663 CGTGCCTGGGAGCTGAAACCACTTGAGCTCTGAGCCCTGACCAAGTACTTCTCCAGA 3722
QY 636 AGATGATGACTTCTGAGCTGTAAGAGAGCTGACAGAGCTGCTATGAGCTTACAGCAAG 695
DB 3723 AGATGAGAGACTTCTGAGCTGTAAGAGAGCTGACAGAGCTGCTATGAGCTTACAGCAAG 3782
QY 696 ACTTCAACCGGCTTAAGAAAGATGAGAGCTTCCAGAGAGCTTCACTGACCTGACCTTGG 755
DB 3783 ACTTCAACCGGCTTAAGAAAGATGAGAGCTTCCAGAGAGCTTCACTGACCTGACCTTGG 3842
QY 756 AGGACATGAGTTTCTGAGCTTGAACCTT 783
DB 3843 GGGCTCATGCTTCTGAGCTTGAACCTT 3870
RESULT 11
US-09-106-182-7
Sequence 7, Application US/09106182
Patent No. 6046035
GENERAL INFORMATION:
APPLICANT: Shi, Yangu
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Cardiotrophin-Like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF385
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-106-182-7
Query Match 6.3%; Score 52; DB 3; Length 396;
Best Local Similarity 85.3%; Pred. No. 0.00011;
Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 716 AAGATGAGCCTCCAGAGCTTCAAGTCACTGACCTTGAAGGAGCAATGTTCTGACT 775
DB 4 ACAGAGAGCCTCCAGAGCTTCAAGTCACTGACCTTGAAGGAGCAATGTTCTGACT 63
QY 776 CTGACCTT 783
DB 64 CTGACCTT 71

FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 137..138
OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED"
US-08-792-019B-3

Query Match 52.5%; Score 429.6; DB 1; Length 5087;
Best Local Similarity 90.4%; Pred. No. 2.8e-103;
Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

276 ACCGTAACCTACCTGGGGCCCCCTTTCAACGAGCCTGACTTCAATCCTCCTGACTGGGG 335
3363 AGCTGAACCTACCTGGGGCCCCCTTTCAACGAGCCTGACTTCAATCCTCCTGACTGGGG 3422
336 CAGAACTCTGCCCCGAGGCGCAAGCTTGAAGTGTGGGGAAGCTTCAATGACAGGC 395
3423 CAGAACTCTGCCCCGAGGCGCAAGCTTGAAGTGTGGGGAAGCTTCAATGACAGGC 3482
336 TCGGCTGACCCAGAACTATGAGGCGTACAGTCACTCTGTTACTTGGGCGTCA 455
3483 TCGGCTGACCCAGAACTATGAGGCGTACAGTCACTCTGTTACTTGGGCGTCA 3542
456 ACCGTGAGGCTGCAACAGCTGAACTCCGACGTAGCCTGGCCCACTTCTGTACAGCCTCC 515
3543 ACCGTGAGGCTGCAACAGCTGAACTCCGACGTAGCCTGGCCCACTTCTGTACAGCCTCC 3602
516 AGGCGCTGCTGGGCGAGCATTTGAGGTGTCATGCGGCAAGCTTGGCTACCACTGCCCCAGC 575
3603 AGGCGCTGCTGGGCGAGCATTTGAGGTGTCATGCGGCAAGCTTGGCTACCACTGCCCCAGC 3662
576 CTCTGCGAGGAGCTAGAGCCAGCTGGGGCCCCCTGGCCCAAGTGACTTCTCCCA 635
3663 CTCTGCGAGGAGCTAGAGCCAGCTGGGGCCCCCTGGCCCAAGTGACTTCTCCCA 3722
636 AGATGATGACTTCTGCTGCTGTAAGAGAGCTGCAAGCTGCTATGAGCTTTCAGCCAGG 695
3723 AGATGATGACTTCTGCTGCTGTAAGAGAGCTGCAAGCTGCTATGAGCTTTCAGCCAGG 3782
696 ACTTCAACCGGCTTAAAGAAAGATGACAGCTTCCAGAGCTTCACTGACCTTGG 755
3783 ACTTCAACCGGCTTAAAGAAAGATGACAGCTTCCAGAGCTTCACTGACCTTGG 3842
756 AGGCAATGCTTTCTGACCTTGAACCT 783
3843 GGGCTCATGGCTTGTGACTTCTGACCTT 3870

RESULT 9
US-08-988-819-3
Sequence 3, Application US/0898819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS

STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 137..138
OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED"
US-08-988-819-3

Query Match 52.5%; Score 429.6; DB 3; Length 5087;
Best Local Similarity 90.4%; Pred. No. 2.8e-103;
Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

276 ACCGTAACCTACCTGGGGCCCCCTTTCAACGAGCCTGACTTCAATCCTCCTGACTGGGG 335
3363 AGCTGAACCTACCTGGGGCCCCCTTTCAACGAGCCTGACTTCAATCCTCCTGACTGGGG 3422
336 CAGAACTCTGCCCCGAGGCGCAAGCTTGAAGTGTGGGGAAGCTTCAATGACAGGC 395
3423 CAGAACTCTGCCCCGAGGCGCAAGCTTGAAGTGTGGGGAAGCTTCAATGACAGGC 3482
336 TCGGCTGACCCAGAACTATGAGGCGTACAGTCACTCTGTTACTTGGGCGTCA 455
3483 TCGGCTGACCCAGAACTATGAGGCGTACAGTCACTCTGTTACTTGGGCGTCA 3542
456 ACCGTGAGGCTGCAACAGCTGAACTCCGACGTAGCCTGGCCCACTTCTGTACAGCCTCC 515
3543 ACCGTGAGGCTGCAACAGCTGAACTCCGACGTAGCCTGGCCCACTTCTGTACAGCCTCC 3602
516 AGGCGCTGCTGGGCGAGCATTTGAGGTGTCATGCGGCAAGCTTGGCTACCACTGCCCCAGC 575
3603 AGGCGCTGCTGGGCGAGCATTTGAGGTGTCATGCGGCAAGCTTGGCTACCACTGCCCCAGC 3662
576 CTCTGCGAGGAGCTAGAGCCAGCTGGGGCCCCCTGGCCCAAGTGACTTCTCCCA 635
3663 CTCTGCGAGGAGCTAGAGCCAGCTGGGGCCCCCTGGCCCAAGTGACTTCTCCCA 3722
636 AGATGATGACTTCTGCTGCTGTAAGAGAGCTGCAAGCTGCTATGAGCTTTCAGCCAGG 695
3723 AGATGATGACTTCTGCTGCTGTAAGAGAGCTGCAAGCTGCTATGAGCTTTCAGCCAGG 3782
696 ACTTCAACCGGCTTAAAGAAAGATGACAGCTTCCAGAGCTTCACTGACCTTGG 755
3783 ACTTCAACCGGCTTAAAGAAAGATGACAGCTTCCAGAGCTTCACTGACCTTGG 3842
756 AGGCAATGCTTTCTGACCTTGAACCT 783
3843 GGGCTCATGGCTTGTGACTTCTGACCTT 3870

Qy	605	CTGGGCGCCCTGGCCACAGTAGCTTCCCTCCAGGAAGATGATGACTTCTGGCTCTCAAGAG	664
Db	600	CTGGGCGCCCTGGCCACAGTAGCTTCCCTCCAGGAAGATGAGACTTCTGGCTCTCAAGAG	655
Qy	665	CTGCAGACCTGGCTATGAGCGTTTCAGCCCAAGCACTTCAACCGGCTTAAGAAAGATGCAG	724
Db	660	CTGCAGACCTGGGCTGTGGCGCTCTGGCCAAAGCACTTCAACCGGCTTAAAGAAAGATGCAG	719
Qy	725	CTTCACAGCAGCTTCAAGTCAACCCCTGCACCTTGAAGGACATGGTTTCTGACCTCTGACCT	783
Db	720	CTTCACAGCAGCTCAAGTCAACCCCTGCACCTGGGGGGCTCATGGCTTCTGACCTTCTGACCT	778

RESULT 7
US-09-106-182-1
; Sequence 1, Application US/09106182

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GENERAL INFORMATION:
APPLICANT: Shi, Yanguu
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Cardiotrophin-like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P3985
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1710 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 46..720
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 46..126
FEATURE:
NAME/KEY: mac_peptide
LOCATION: 127..720
US-09-106-182-1

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Query Match	Score	DB	Length
76.6%	627	3	1710

Best Local Similarity 91.74; Pred. No. 3.8e-155;
Matches 674; Conservative 0; Mismatches 60; Indels 1; Gaps 1

49 GCCTCTGGAGAGAGCCGCCGCCGCCGCCGCCAGCCCATGTGACTCCGAGC 108

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Oy	109	AGGGGACTGTGGGGATGTTATGCTTGCCCTATGACAGGTGCTGGGCACTCTCTCGACT	168
Db	60	AGGGGACTGATGGGGATGTTATGCTGTGCTGTGACAGGTGTCTCGGACACTCTCTCGAGT	119
Oy	169	GGCAGCTCTTAAATCGCAGCAGAGATTCAGAGGCCCTGGGCCCTCCATCCAGAAAACCTATGA	228
Db	120	GCCAGCTCTCAATCGCAGGGGAGCCAGGGGCTGGGCCCTCTCCATCCAGAAAACCTATGA	179
Oy	229	CCTCACCCGCTACTTGGAGATCAACTCCGAGCTGTAGCTGGGACTTACCTGAACTACT	288
Db	180	CTCACCCGCTACTTGGAGACCAACTCCGAGCTGTGGACTTATCTGAATACTCT	239
Oy	289	GGGGCCCCCTTTCAACGAGCTGACTTCAATCTTCCTGACTGGGGGCAAGAACTCTGCC	348
Db	240	GGGCCCCCTTTCAACGAGCTGACTTCAACCTTCGCCGCTGGGGGCAAGAACTCTGCC	299
Oy	349	CAGGGGCAAGGTCACTTGGAGATGTGGCGAAGGCTCAATACAGGCTGGCGGCTGACCA	408
Db	300	CAGGGGCACTGTGACTTGGAGATGTGGCGAAGGCTCAATACAACTGGCGGCTGACCA	359
Oy	409	GAACATAAGAGCGTACAGTCACTCTGTGTTACTTGGGTGGCTCAACCGTCAGCTGC	468
Db	360	GAACATAAGAGCGCTACAGCACTCTGTGTTACTTGGGTGGCTCAACCGTCAGCTGC	419
Oy	469	CACAGCTGAATCTCCGACGTAGCTGGGCCCACTCTTGTATACAGCCTCGAGGCTGTGGG	528
Db	420	CACGTGTGAGCTGGCGGCGGACGCTGGGCCCACTTGTGACACAGCTCCAGGGCTGTGGG	479
Oy	529	CACCAATTGCAGGTGTCAATGGCGACGCTTGGCTAACCACTGGCCGACGCTCTGGCAGGGAC	588
Db	480	CACCAATTGGGGGTCTATGGCAGCTCTGGGCTTACCACTGGCCGACGCTGTGGGAC	539
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Db	660	CAAGAAAGAAATGCAAGCTTCCAGCAGCTGCAATCACTCTGCACTTGGGGGCTCATGGCTT	719
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RESULT 8
US-08-79

; Sequence 3, Application US/08792019E
; Patent No. 5741772

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; GENERAL INFORMATION:
; APPLICANT:  CHANG,

```

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; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
;
; NUMBER OF SEQUENCES: 16

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.

STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS

STATE: CA
COUNTRY: USA

ZIP: 91320
COMPUTER READER

```

MEDIUM TYPE: Floppy
COMPUTER: IBM PC COMP

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0

DATE: 08/08/2008 11:00:00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792 019B

RECEIVED ON APRIL 11, 1961

STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..764
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 171..764
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 90..170
US-08-792-019B-1

Query Match 81.7% Score 669.4; DB 1; Length 797;
Best Local Similarity 92.0%; Pred. No. 2.4e-166;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

5 ATTAAGCTTCCCGGAGCCGCGCTCCCTCCCACTCCGACCTCTGGGAAGAG 64
1 ATTAAGCTTCCCGGAGCCGCGCTCCCTCCCACTCCGACCTCTGGGAAGAG 60
65 CCGGCG 124
61 CCGGCG 119
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120 ATGTTAGGCTGCTGTGCAAGGCTGTGTGCACTTCCCTGCAAGTCCCACTTATGCG 179
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RESULT 5
US-08-988-819-1
Sequence 1, Application US/08988819
Patent No. 6054294

GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUTROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 90..764
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 171..764
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 90..170
US-08-988-819-1

Query Match 81.7% Score 669.4; DB 3; Length 797;
Best Local Similarity 92.0%; Pred. No. 2.4e-166;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

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QY 541 TGTGATGGGAGCGCTGGTGGTACCTGACCTGCCCCAGCCTGTGCGAGGACATGAGCCAGCTG 600
DB 541 TGTGATGGGAGCGCTGGTGGTACCTGACCTGCCCCAGCCTGTGCGAGGACATGAGCCAGCTG 600
QY 601 GGGCCCTGGCCCTGGCCCAAGTACTTCTCCGAAAGATGATGACTTCTGGCTGTGAA 660
DB 601 GGGCCCTGGCCCTGGCCCAAGTACTTCTCCGAAAGATGATGACTTCTGGCTGTGAA 660
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RESULT 3
US-09-016-534-4

Sequence 4, Application US/09016534
Patent No. 613874

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI
APPLICANT: ELLIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/792,019

FILING DATE: 03-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31,602

REFERENCE/DOCKET NUMBER: A-442B

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 819 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 95..769

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 176..769

FEATURE:

NAME/KEY: sig_peptide

LOCATION: 95..175

FEATURE:

LOCATION: 95..175

US-09-016-534-4

Query Match 100.0%; Score 819; DB 3; Length 819;
Best Local Similarity 100.0%; Pred. No. 1.5e-205;
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATATTAAAGCTTGGCCGAGCCGCGCTGCGCTCCCACTCCGACCTCTGGGAGA 60
DB 1 TATATTAAAGCTTGGCCGAGCCGCGCTGCGCTCCCACTCCGACCTCTGGGAGA 60
QY 61 GGAGCCGCGCCG 120
DB 61 GGAGCCGCGCCG 120
QY 121 GGAGATGTTAGCTTGGCTTATGACAGGTGCTGAGACCTCCCTGCACTGCTTAA 180
DB 121 GGAGATGTTAGCTTGGCTTATGACAGGTGCTGAGACCTCCCTGCACTGCTTAA 180
QY 181 TCGACAGGAGATCCAGGCGCTGCGCGCTGCAATCCAGAAACCTATGACCTCA 240
DB 181 TCGACAGGAGATCCAGGCGCTGCGCGCTGCAATCCAGAAACCTATGACCTCA 240
QY 241 CCTGAGAGATCAACTCCGAGCTTAGCTGAGGAGCTAAGCTAAGCTGAGGCGCCCTTT 300
DB 241 CCTGAGAGATCAACTCCGAGCTTAGCTGAGGAGCTAAGCTAAGCTGAGGCGCCCTTT 300
QY 301 CAACGAGCTGACTTCAATCTCTCTGAGCTGAGGAGGAGAACTCTGAGGAGGAGAGCT 360
DB 301 CAACGAGCTGACTTCAATCTCTCTGAGCTGAGGAGGAGAACTCTGAGGAGGAGAGCT 360
QY 361 CAACTTGAAGTGTGCGGAGGAGCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGG 420
DB 361 CAACTTGAAGTGTGCGGAGGAGCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGG 420
QY 421 GTACAGTACCTCTCTGTGTATTTAGCTGAGGAGGAGCTCAAGCTGAGGAGCTGAGT 480
DB 421 GTACAGTACCTCTCTGTGTATTTAGCTGAGGAGGAGCTCAAGCTGAGGAGCTGAGT 480
QY 481 CCGAGTACCTCTGAGGAGGAGCTTGTACAGGAGCTTCAAGGAGGAGCTGAGGAGGAGT 540
DB 481 CCGAGTACCTCTGAGGAGGAGCTTGTACAGGAGCTTCAAGGAGGAGCTGAGGAGGAGT 540
QY 541 TGTGATGGGAGCGCTTGGCTTACCACTGCGCGGAGCTTGGAGGAGCTGAGCCAGCTG 600
DB 541 TGTGATGGGAGCGCTTGGCTTACCACTGCGCGGAGCTTGGAGGAGCTGAGCCAGCTG 600
QY 601 GGGCCCTGGCCCTGGCCCAAGTACTTCTCCGAAAGATGATGACTTCTGGCTGTGAA 660
DB 601 GGGCCCTGGCCCTGGCCCAAGTACTTCTCCGAAAGATGATGACTTCTGGCTGTGAA 660
QY 661 GGAGCTGACAGACTGCTATGAGCTTCAAGCCAGGACTTCAACCGGCTTAAGAAAGAT 720
DB 661 GGAGCTGACAGACTGCTATGAGCTTCAAGCCAGGACTTCAACCGGCTTAAGAAAGAT 720
QY 721 GGAGCTTCCAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 780
DB 721 GGAGCTTCCAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 780
QY 781 CCTTAACCCCAACCTCCAGGCCCCAGTCACTGTGCTT 819
DB 781 CCTTAACCCCAACCTCCAGGCCCCAGTCACTGTGCTT 819

RESULT 4

US-08-792-019B-1

Sequence 1, Application US/08792019B

Patent No. 5741772

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI

TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSER: AMGEN INC.

STREET: 1840 DEHAVILLAND DRIVE

CITY: THOUSAND OAKS


```

OY 1 TATTATTAAGCTTGGCCGAGCCGCGGCTGCTCCCACTCCGCGCAGGCTCTGGAGGA 60
DB 1 TATTATTAAGCTTGGCCGAGCCGCGGCTGCTCCCACTCCGCGCAGGCTCTGGAGGA 60
OY 61 GAGGCGGCGCCGCGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120
DB 61 GAGGCGGCGCCGCGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120
OY 121 GGGGATGTTAGCTTGGCTATGACAGGCTGTGTGGCACTCTCCCTGAGAGTCCAGCTTTAA 180
DB 121 GGGGATGTTAGCTTGGCTATGACAGGCTGTGTGGCACTCTCCCTGAGAGTCCAGCTTTAA 180
OY 181 TCGCAGAGAGATCCAGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCTTA 240
DB 181 TCGCAGAGAGATCCAGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCTTA 240
OY 241 CTTGGAGCATCACTCCGAGCTTAGCTGTGGAGCTTACCTGAACTTACCTGGGGGCCCCCTTT 300
DB 241 CTTGGAGCATCACTCCGAGCTTAGCTGTGGAGCTTACCTGAACTTACCTGGGGGCCCCCTTT 300
OY 301 CAACGAGCTGACTTCAATCTCTCTGACTGGGGGCAAGAACTCTGCCAGGCGCCAGCGT 360
DB 301 CAACGAGCTGACTTCAATCTCTCTGACTGGGGGCAAGAACTCTGCCAGGCGCCAGCGT 360
OY 361 CAACCTTGGAGTGTGGCGAGGCTCAATGACAGGCTGTGGGCTGAGCCAGAACTTATGAGGC 420
DB 361 CAACCTTGGAGTGTGGCGAGGCTCAATGACAGGCTGTGGGCTGAGCCAGAACTTATGAGGC 420
OY 421 GTACAGTCACTCTGTGTTACTTCTGCTGCTGCTCAACCGTCAAGGCTGCGCACAGCTGAACT 480
DB 421 GTACAGTCACTCTGTGTTACTTCTGCTGCTGCTCAACCGTCAAGGCTGCGCACAGCTGAACT 480
OY 481 CCGAGCTGAGCTGCGCCCACTTCTGTAACAGGCTCCAGGCGCTGCTGGGCGAGATTCGACG 540
DB 481 CCGAGCTGAGCTGCGCCCACTTCTGTAACAGGCTCCAGGCGCTGCTGGGCGAGATTCGACG 540
OY 541 TGTCAATGGGAGAGCTTGGCTTACCACTGCGCCGAGCTGCGCAGGAGCACTGAGCCAGCGTG 600
DB 541 TGTCAATGGGAGAGCTTGGCTTACCACTGCGCCGAGCTGCGCAGGAGCACTGAGCCAGCGTG 600
OY 601 GGGCCCTGGCCCTGCGCCAGAGTACTTCTCCAGAAATGATGACTTCTGCTGCTGTA 660
DB 601 GGGCCCTGGCCCTGCGCCAGAGTACTTCTCCAGAAATGATGACTTCTGCTGCTGTA 660
OY 661 GAGAGCTGAGAGCTTGGCTTATGAGCTTCAAGCAAGACTTCAACCGGCTTAAAGAAAGAT 720
DB 661 GAGAGCTGAGAGCTTGGCTTATGAGCTTCAAGCAAGACTTCAACCGGCTTAAAGAAAGAT 720
OY 721 GCAGCTCCAGAGCTTCAAGTCACTGACCTTGAAGGAGCATGGTTCTGACTCTGAC 780
DB 721 GCAGCTCCAGAGCTTCAAGTCACTGACCTTGAAGGAGCATGGTTCTGACTCTGAC 780
OY 781 CTTTAAACCCCAACCTCCAGGCGCCAGCTGCTGCTT 819
DB 781 CTTTAAACCCCAACCTCCAGGCGCCAGCTGCTGCTT 819

```

RESULT 2

```

US-08-988-819-4
; Sequence 4, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 95..769
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 176..769
; FEATURE:
; NAME/KEY: s1g_peptide
; LOCATION: 95..175
; US-08-988-819-4

Query Match 100.0%; Score 819; DB 3; Length 819;
Best Local Similarity 100.0%; Pred. No. 1.5e-205;
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TATTATTAAGCTTGGCCGAGCCGCGGCTGCTCCCACTCCGCGCAGGCTCTGGAGGA 60
DB 1 TATTATTAAGCTTGGCCGAGCCGCGGCTGCTCCCACTCCGCGCAGGCTCTGGAGGA 60
OY 61 GAGGCGGCGCCGCGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120
DB 61 GAGGCGGCGCCGCGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120
OY 121 GGGGATGTTAGCTTGGCTATGACAGGCTGTGTGGCACTCTCCCTGAGAGTCCAGCTTTAA 180
DB 121 GGGGATGTTAGCTTGGCTATGACAGGCTGTGTGGCACTCTCCCTGAGAGTCCAGCTTTAA 180
OY 181 TCGCAGAGAGATCCAGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCTTA 240
DB 181 TCGCAGAGAGATCCAGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCTTA 240
OY 241 CTTGGAGCATCACTCCGAGCTTAGCTGTGGAGCTTACCTGAACTTACCTGGGGGCCCCCTTT 300
DB 241 CTTGGAGCATCACTCCGAGCTTAGCTGTGGAGCTTACCTGAACTTACCTGGGGGCCCCCTTT 300
OY 301 CAACGAGCTGACTTCAATCTCTCTGACTGGGGGCAAGAACTCTGCCAGGCGCCAGCGT 360
DB 301 CAACGAGCTGACTTCAATCTCTCTGACTGGGGGCAAGAACTCTGCCAGGCGCCAGCGT 360
OY 361 CAACCTTGGAGTGTGGCGAGGCTCAATGACAGGCTGTGGGCTGAGCCAGAACTTATGAGGC 420
DB 361 CAACCTTGGAGTGTGGCGAGGCTCAATGACAGGCTGTGGGCTGAGCCAGAACTTATGAGGC 420
OY 421 GTACAGTCACTCTGTGTTACTTCTGCTGCTGCTCAACCGTCAAGGCTGCGCACAGCTGAACT 480
DB 421 GTACAGTCACTCTGTGTTACTTCTGCTGCTGCTCAACCGTCAAGGCTGCGCACAGCTGAACT 480
OY 481 CCGAGCTGAGCTGCGCCCACTTCTGTAACAGGCTCCAGGCGCTGCTGGGCGAGATTCGACG 540
DB 481 CCGAGCTGAGCTGCGCCCACTTCTGTAACAGGCTCCAGGCGCTGCTGGGCGAGATTCGACG 540

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RESULT 13

B75332

extracellular solute-binding protein, family 5 - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C/Accession: B75332

M. White, O.; Eisen, J.A.; Heibelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A/Reference number: A75250; PMID:20036896; PMID:10567266

A/Accession: B75332

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-520 <WHI>

A/Cross-references: GB:AE002034; GB:AE000513; NID:G6459742; PIDN:AAFI1508.1; PID:G645974

A/Experimental source: strain R1

C/Genetics:

A:Gene: DR1955

A:Map position: 1

C:Superfamily: dipeptide transport protein

Query Match

Best Local Similarity 23.3%; Score 85; DB 2; Length 520;

Matches 40; Conservative 20; Mismatches 54; Indels 58; Gaps 7;

DB 19 LNHLPVAPALNRTGDPGPGSIQ-----FNPRPGAETLPRAVTLVWRSLSN-DRLNLTN 106

DB 363 LMY-----PSISRYLPTPKVFAEAIADLGAIGIKVNLKEDPDKYLRAGVFMQY 418

DB 107 YEAVSHLCYLRGLNRQAATAEIRSLAHFCTSLQG-----LLGSIAQVMTLG 155

DB 419 GNGGDNDPDNDFYSAYGKGSDDIGFNP-----NLTNTLTKGRALTYA 464

DB 465 QQR-----PYKQHLHLYTNANVRLPLVHSTAPAAARTYKGMITGPISIVG 511

DB 107 YEAVSHLCYLRGLNRQAATAEIRSLAHFCTSLQG-----LLGSIAQVMTLG 155

DB 465 QQR-----PYKQHLHLYTNANVRLPLVHSTAPAAARTYKGMITGPISIVG 511

DB 107 YEAVSHLCYLRGLNRQAATAEIRSLAHFCTSLQG-----LLGSIAQVMTLG 155

DB 465 QQR-----PYKQHLHLYTNANVRLPLVHSTAPAAARTYKGMITGPISIVG 511

DB 107 YEAVSHLCYLRGLNRQAATAEIRSLAHFCTSLQG-----LLGSIAQVMTLG 155

DB 465 QQR-----PYKQHLHLYTNANVRLPLVHSTAPAAARTYKGMITGPISIVG 511

DB 107 YEAVSHLCYLRGLNRQAATAEIRSLAHFCTSLQG-----LLGSIAQVMTLG 155

DB 465 QQR-----PYKQHLHLYTNANVRLPLVHSTAPAAARTYKGMITGPISIVG 511

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DB 107 YEAVSHLCYLRGLNRQAATAEIRSLAHFCTSLQG-----LLGSIAQVMTLG 155

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DB 107 YEAVSHLCYLRGLNRQAATAEIRSLAHFCTSLQG-----LLGSIAQVMTLG 155

DB 478 LL-----LPLALPSPPEWNG-----RAEVRVLDVGGGLAVLVTRB-----HVLVDSG 522

DB 120 LNRQAA-----TAEIRSLAHFCTSLQGLSIAQVMTLGYP-----PQ 160

DB 523 A-RQGAFFMGERRVVPVLRSLDR-----LDGLLSHNDNDHAGAPVYASRPV 573

DB 161 PLPGTEPAPAPGPAHSDFLQKDDFWLLKEQLTWLRSAKDFNRLKKQPPAASVTLHL 220

DB 574 WIVSGEPALPPLFADSCDERSWSDVGVFQMAWAQGDND-----DRSCVLAV 624

DB 221 EAHG 224

DB 625 EADG 628

RESULT 15

T35231

hypothetical protein SC5C7.24c SC5C7.24c - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999

C/Accession: T35231

R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1998

A/Reference number: Z21572

A/Accession: T35231

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-272 <SEB>

A/Cross-references: EMBL:AL031515; PIDN:CAA20636.1; GSPDB:GN00070; SCOEDB:SC5C7.24c

A/Experimental source: strain A3(2)

C/Genetics:

A:Gene: SCOEDB:SC5C7.24c

Query Match

Best Local Similarity 23.9%; Score 83; DB 2; Length 272;

Matches 38; Conservative 15; Mismatches 50; Indels 56; Gaps 7;

DB 23 PAVPALN-----RTGDPGPGSIQKTYDLTRYLEHQLRSLAGTYLNYLGPEN----- 70

DB 95 PALGALREGMERLIGYEYFPAVVDATRYVLAARGLAMMDGVAEHLLTPPLNARLT 154

DB 71 -EPDFNPRLGAETLPRAVTLVWRSLSNDRRLTONTVEAVSHLCYLRGLNRQAATAE 129

DB 155 LHPDGLAPRIR-----NLREWR-----GHL-----EGM 178

DB 130 RSLA-HFCTSLQGLSIAQVMTLGYPPLPPTER 167

DB 179 ERQIALHRSRPLRELYDEVA-----AYFVPEVSGAEP 211

Search completed: February 9, 2004, 06:17:42

Job time : 18 secs

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A:Cross-references: GB:AE004483; GB:AE004091; NID:G9946313; PIDN:AA0G3843.1; GSPDB:GN00
A:Experimental source: strain PA01
A:GeneticB:
A:Gene: PA0454
C:Superfamily: hypothetical protein H11680

Query Match          7.3%; Score 89; DB 2; Length 733;
Best Local Similarity 25.8%; Pred. No. 4;
Matches 57; Conservative 26; Mismatches 64; Indels 74; Gaps 13;

QY  28  LNRITGDPGPGSIOKTYDLTRYLE-----HQLSLAGTYLVLYGPFNEPD--FNRP 77
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  230  LNRIGHGPRGKRV-----SRYLKLYFIADVDHEAASSHHFYRNLAEAFPHSDVLPFCQ 283
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  78  RL-----GAEFLPRATVNLVSWRSLSNDRLLTONYEAVSHLQCYLRGLNQAAVTAELRR 131
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  284  RLNQOGKACQALARA-----IRLRQFPD--YA-----DRELLEDLQA 320
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  132  SLAHP-----CTSLQGL--LGSVAGVATLGVLPQPLPGRTPAMAPGPAISDFLQKDD 184
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  321  SLEHTRQGSNPAWKGSLRSLGALANLTTLRKL-----AGASNPDAIADQD 368
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  185  FWLKEIQWLMRSKAD--FNRLKKKKQPPAASVTLHLPAHG 224
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  369  SALDDRSP-----RLSKDAFERLRQOUTP-----TSLPRHG 400
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 10
 T38943
 probable guanine nucleotide binding protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38943
 R:Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, May 1997
 A:Reference number: Z21819
 A:Accession: T38943
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1113 <SKE>
 A:Cross-references: EMBL:Z95396; PIDN:CAB08769.1; GSPDB:GN00066; SPDB:SPAC57A7.11
 A:Experimental source: strain 972h; cosmid C57A7
 C:Genetics:
 A:Gene: SPDB:SPAC57A7.11
 A:Map position: 1

	Query Match	7.0%; Score 86; DB 2; Length 133;
	Best Local Similarity	22.2%; Pred. No. 16;
	Matches	58; Conservative 31; Mismatches 84; Indels 89; Gaps 12.
Oy	15 LCTVLMHLPAY--PALNR-----TGDPGPGPSI-----OKTYDLTRYLEHQRS	56
Dd	811 LAPFLQHPALPKASLSDKDTDNSTSPDKPAPFVSSENKLINRSLSTRSLKGLALS	870
Oy	57 LAG-----TLYNYL-----GPP-FNEPDFNPRLGAETLRPATYANL	91
Dd	871 LAGSDRASSELLSINGENKPRAESNNLHLTSAKYAPGPAAENELEYO----SELDMLPTLSLF	926
Oy	92 EWMFSLNDRLRLTONYEAYSHLLCYLRGL--NROAATAEILRSIAHFCTS-----LOG	142
Dd	927 DMSRYCTPEPMQRPNEDDEPGSICYNORIMRRNRBEKLIYRTPLAEYSTNGRNNOQLMT	986
Oy	143 LLGSIGAMATIGVYLPQPLPCTEPBPAMA.PGPASHPLCKMDPFWLKE---LQTWLMRSA	199
Dd	987 FNNNTIA-----PRKLMFHQPQQDILITLGKDIIQVWDWRN	1022
Oy	200 KDFNRLLKKGMPPPAASVTTLHL	220
Dd	1023 RCLNSFPK-----TSASATTNV	1038

Probable cytosolic gamma-synthase APE2068 - Acetopyrum pernix (strain K1)
 C.Species: Acetopyrum pernix
 C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C.Accession: F72511
 R.RikawaDagashi, Y., Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa, Res. 6, 83-101, 1999
 A.Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Acetopyrum pernix
 A.Reference number: A72450; MUID:99310339; PMID:10382966
 A.Accession: F72511
 A.Status: Preliminary
 A.Molecule type: DNA
 A.Residues: 1-389 <KAW>
 A.Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BA81078.1; PID:95105766
 A.Experimental source: strain K1
 C.Genetics:
 A.Gene: APE2068
 C.Superfamily: O-succinylhomoserine (thiol)-lyase

Query Match	7.0%	Score 85.5;	DB 2;	Length 389;
Best Local Similarity	22.9%	Pred. No. 3.8;		
Matches	47;	Conservative	20;	Mismatches 77;
			Indels	61;
			Gaps	8

QY	43	TYDLTRYIEHOLRSIAGTYLNYLCGPENEPDPNPRLGAETLPRAVTNIEVWRSI----	97
DB	107	TYGGSTRSLLEMLSSITGIEVRLGAPWMD-----LLDIDVCWADIIIVES	150
QY	98	--NDRILRTQNYEAVSHLCTLRGINRQAAVLELR-----RSI---AHFCTS	139
DB	151	MANPLLRPP-----LSGIYRAGSGGVAVVVDNTPATPIAIVRLRGAAH--S	197
QY	140	LOGLLGSIAGMATLGYPLPQPL--PGTEPAAVAPGASDFLOKMDFWMLKELQTMWRS	198
DB	198	LESITKTYIAGNDVVGSLGRVEEDLEPLNMNRKILGTIQPIDAY-----LAWRG	249
QY	199	AKDFNRLKKKQNPAASTYTLHLEAH	223
DB	250	MKTLKARFEAOSRAAVEVAEWLESH	274

RESULT 12
C38604 poly(3-hydroxyalkanoate) polymerase (EC 2.7.7.-) 3 - Pseudomonas oleovorans
C:Species: Pseudomonas oleovorans
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Sep-2000
A:Accession: C38604
R:Huisman, G.W.; Monnik, E.; Meima, R.; Kazemier, B.; Terpstra, P.; Miltolt, B.
J. Biol. Chem. 266, 2191-2198, 1991
A:Title: Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas oleovorans. Identit
A:Reference number: A38604; PMID:9115830; PMID:1989978
A:Accession: C38604
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-560 <HUI>
A:Cross-references: GB:MS8445; NID:g151441; PIDN:AA25934.1; PID:g151444
C:Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C:Keywords: nucleotidyltransferase

	Query Match	7.0%	Score 85.5;	DB 2,	length 560;	
	Best Local Similarity	30.2%	Pred. No. 6;			
	Matches	38;	Conservative	16;	Mismatches	43; Indels 29; Gaps 7
OY	77 PRLGAETLPRAATVNIIEWRSLNDRILRLQNTVEAASHLCLYGLGRQAATAELRRSL--A	134				
Dd	5 PAKGTPTPLPAISMNVQ-----NALIGLRGR-----DLSTLRNVRQS-----LRHPHLYA	50				
OY	135 HFCISLOGGASINGWATLCYPLPQLPG---TEPAWAPGPAAHSDFLOKDDFWLKE	190				
Dd	51 HHLLALGGQLGRV-----ILGDTPQWPBPDPSPSDPTWSQNPFRRGIQA-----YLAWQ	101				
OY	191 LQTWLW	196				
Dd	102 KOTRLW	107				

Db 267 DDEDESADKEDDEAVKOL-----SEKDL--LKRHIE 298

RESULT 6

G02312
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C/Accession: G02312
R:Wood, W.I.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01035

A/Accession: G02312

A/Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-201 <MOO>

A:Cross-references: EMBL:U43030; NID:g1151149; PID:g1151150

C:Genetics: GDB:CTF1; CT-1

A:Gene: GDB:CTF1; CT-1

A:Cross-references: GDB:567078

A:Map position: 1p22-1p22

Query Match

Best Local Similarity 25.7%; Score 91.5; DB 2; Length 201;

Matches 45; Conservative 23; Mismatches 92; Indels 15; Gaps 5;

Db 144 GAANRGPRAEPAYASA--ASATGVFAKVIAGLVCGLYRWMISRTGDLGQL 195

RESULT 7

JH0680
ciliary neurotrophic factor - chicken

N:Alternate names: growth-promoting activity protein

C:Species: Gallus gallus (chicken)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000

C/Accession: JH0680; P00057

R:Leung, D.W.; Parent, A.S.; Cachianes, G.; Esch, F.; Coulombe, J.N.; Nikolics, K.; Ecker

A:Title: Cloning, expression during development, and evidence for release of a trophic f

A:Reference number: JH0680; PMID:92304573; PMID:1610564

A:Accession: JH0680

A:Molecule type: mRNA

A:Residues: 1-195 <LEU>

A:Cross-references: GB:M80827; NID:g211822; PIDN:AAA48784.1; PID:g211823

A:Experimental source: eye

R:Eckstein, F.P.; Esch, F.; Holbert, T.; Blacher, R.W.; Nishi, R.

Neuron 4, 623-631, 1990

A:Title: Purification and characterization of a trophic factor for embryonic peripheral

A:Reference number: P00057; PMID:90211978; PMID:2322465

A/Accession: P00057

A:Molecule type: protein

A:Residues: 155-166, 'X', 168-175 <ECK>

A:Experimental source: sciatic nerves

C:Comment: This is a neurotrophic protein.

C:Superfamily: ciliary neurotrophic factor

C:Keywords: growth factor

Db 23 LARKRSDVTLIDIVYERQ-----LDASISVAADVGPVTA--ERNAEQGTQRLID 75

QY 106 N---YEYSHLCTYRGLNRQA--ATAELRSIA-----HPTSLQGLGSLGVMA 152

Db 76 NLAAVAFRTLAQMLEEQRRLGDTDAELGPALAMLLQVSAFYTHEEL-----ELE 130

QY 153 TLGYPPLQPLPGTEPAMAPGPAHSDFLQKMDPFWLKEQLTWLMSAKDPNLLKKKQPP 212

Db 131 SGAPAFEE---GSEPP-AP-PRLSLFEQLRGURVRLAQVAVRSVRRLRLQSK--HGQ 183

QY 213 AASVTIHL 220

Db 184 GSGAALGL 191

RESULT 8

F82965
hypothetical protein PA5441 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C/Accession: F82965

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: AB2950; PMID:20437337; PMID:10984043

A:Accession: F82965

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-733 <STO>

A:Cross-references: GB:AE004957; GB:AE004091; NID:g9951770; PIDN:AA008826.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics: PA5441

A:Gene: PA5441

Query Match

Best Local Similarity 23.9%; Score 90; DB 2; Length 733;

Matches 48; Conservative 24; Mismatches 81; Indels 48; Gaps 8;

Db 23 PAVPALNRTGDPGPPSIQKTYDLTRYLEHQIRSLAGTYLNYLGPPEPDPNPRLAG 82

QY 102 PALPASEAETPPAPAPSPALAEIAR-----OMGAE 132

Db 83 TLPRATVLEWRSINDRLRLTQNEAYSHLCTYRGLNRQAATAELR--RSIAHCTSIQ 141

QY 133 ALPEKIAAGEFEGEGSRCSNDQSA---LAFRLQV-RDGLGEAETKALAN--SRL 184

Db 142 GLGSLAGVMAITGYPLPQPLPGTEPAMAPGPAHSDFLQKMDPFWLKEQLTWLMSAKD 201

QY 165 DLGACGMEQBELGCVLAQ---GVES--AAGKAFATYLEAANFTSGR-----PDEAQG 234

Db 202 ENRLKKKQPPAPASVTLHLEA 222

QY 235 FKALQDVQSPWLKETATYLIQA 255

RESULT 9

DB3588
conserved hypothetical protein PA0454 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C/Accession: DB3588

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: AB2950; PMID:20437337; PMID:10984043

A:Accession: DB3588

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-733 <STO>

Query Match

Best Local Similarity 27.7%; Score 90; DB 2; Length 195;

Matches 52; Conservative 21; Mismatches 83; Indels 33; Gaps 10;

Db 46 LTRYLEHQIRSLAGTYLNYLGPPEPDPNPRLAGETLPRATVLEWRSINDRLRLTQ 105

C:Keywords: cytokine; glycoprotein
F:164/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 9.0%; Score 110.5; DB 2; Length 203;

Best Local Similarity 27.4%; Pred. No. 0.0083;

Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

40 IOKTYDLFRYLEHQRLSLAGTLYLNLGPPENPDNPRL---GAETLPRAVNLVWRS 96

27 IROTHNLARLLTKVLEQLLEEVYQOGEFGLPGSPPLPLPLAGLSPASHAGLPV--- 83

97 LNDRLRLTONYEAVSHLLCYLRLNROA---TAELRSLAHFCTSLQGLSIAGVM 151

84 -SERLR--QDAALSVLPALDAVRRQELNPRAPRLRLSLJEDARQVRAALGAAYETVL 140

152 ATLGLPRLPPLPTEPA---WAPGPAHSDPLQKMDPWLKELQTLWMSAKPFNL 205

141 AALGAARG--PGPEPVATLFTANSTAGISAKVLGFHVGVLGVEWWSRTGDLGOL 197

RESULT 3

transferase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Sep-2000

C:Accession: T34916

R:Oliver, K.; Harris, D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, January 1998

A:Reference number: 221558

A:Accession: T34916

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-640

A:Cross-References: EMBL:AL021409; PIDN:CAA16181.1; GSPDB:GN00070; SCOEDB:SC3F7.10

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC3F7.10

C:Superfamily: glycine C-acetyltransferase homology

F:287-624/Domain: glycine C-acetyltransferase homology <GCA>

Query Match 7.6%; Score 93.5; DB 2; Length 640;

Best Local Similarity 28.3%; Pred. No. 1.3;

Matches 52; Conservative 12; Mismatches 63; Indels 57; Gaps 9;

22 LPAVALNRTPGPGPSIQKTYDLTRYLEHOL---RSLAGTLYLNLGPPENPDNPRL 78

100 LPAVAP-EGTGDPTVAVAAAMROQYQHQGLGADALEG-----E 140

79 LGAETLPRAVNLVWRS LNDRLRLTONYEAVSHLLCYLRLNROAATAELRSLAHFCT 138

141 LGVDVSVLTSSVAEA---TERLGLT-----GAAPDAAGTTTBALA--D 179

139 SLQGLSIAGVMATLGYPLPPLPCTEPAPAPGPAHSDPLQKMDPWLKELQTLWMS 198

180 ALRGL-----VAAAPGTAVPAPATGAA-APAPRSGNAP-----APGADGMDHRS 225

QY 199 AKDF 202

Db 226 MKDF 229

RESULT 4

hypothetical protein BME110989 [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C:Accession: AD3633

R:DelVecchio, V.G.; Kaparatel, V.; Rodkar, R.J.; Patra, G.; Muir, C.; Los, T.; Ivanova, .; Maur, M.; Goldman, E.; Selikov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letecse, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: AD3633

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-200 <KIR>

A:Cross-References: GB:AE008918; PIDN:PAU54231.1; PID:917985203; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME110989

A:Map position: 11

Query Match 7.6%; Score 92.5; DB 2; Length 200;

Best Local Similarity 23.9%; Pred. No. 0.38;

Matches 55; Conservative 21; Mismatches 89; Indels 65; Gaps 11;

10 GMLACLTVLNLHLPALNRTPGPGPSIQKTYDLTRYLEHOLSLAGTLYLNLGPP 69

2 GLMGALV---LPSLEAKTQDAAPNPATSPHADVY---LRGADIFSTGI--- 51

70 NEPPNPRLGAETLPRAVNLVWRS LNDRLRLTONYEAVSHLLCYLRLNROA 124

52 -----DEIGAE-LQAAGVAHAGHAAMRLVNLRIVADQKQKHLVPLIGSLGANA 103

125 A---TAELRSLAHFCTSLQGLSIAGVMATLGYPLPPLPCT-----EPAN-- 169

104 AIIYAELELR-----GIADVYATFATGDPPLPGVNRVNVNPFYKHQWGWL 151

170 --APGPAHSDPLQKMDPWLKELQTLWMSAKPFNLK--KKMPAPASV 216

152 PLVPEPRFHGLENRD-----FSNAKGVGHNIKORLOAEV 189

RESULT 5

hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: G86182

R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasey, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

A:Authors: Hui, J.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Matli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A66141; MUID:21016719; PMID:11130712

A:Accession: G86182

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-332 <STO>

A:Cross-References: GB:AE005172; NID:97211973; PIDN:AAF40444.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 7.5%; Score 92; DB 2; Length 332;

Best Local Similarity 25.9%; Pred. No. 0.79;

Matches 57; Conservative 24; Mismatches 73; Indels 66; Gaps 12;

23 PAVPALNRTPGPGPSIQKTYDLTRYLEHOLSLAGTLYLVN----- 64

Db 113 PSYVAGNISGYR-PRPSF--TYDEPGYQROMESLQGFIRBNQIRPLRLGSGSPVG 169

QY 65 LGPPNEPDNPRLGAETLPRAVNLVWRS LNDRLRLTONYEAVSHLLCYLRLNROA 124

Db 170 LGPIRASQFLOPRAV---PPPTSLIDTSHNRKRSK-----DEALAVVRG--RKV 215

QY 125 ATAELRSL-----AHFCTSLQGLSIAGVMATLGYPLPPLPCT-----GEPAPMA 170

Db 216 RITBSSSLVYLGNSWLNKGAHV-----GIOPQSGIMK-----PLPKPLPVDTTETISVP 266

QY 171 PGPAHSDPLQKMDPWLKELQTLWMSAKPFNLKKKQ 210

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Query	Match	Similarity	Score	DB	Length
18	VLWHLPAVPAL	-----NRTGDPGPGPSIOKTYDLYLHQLRSIAGTYLNYLGP	67		
6	LWLWLLPILLSIAAVGSGMGTCGRAGSPRAGSPLOPREPLS	-----YSRLQRKSLA	55		
68	PFNEDFNPPRLGAETLPRATVNLVWRSIINDRLRLTONYEAYSH	-----LI-CYLRGLNRQAA	126		
56	-----VDFVVPBL	-----FRVYARDLLLPSSSELKAGR	84		
127	AELRSLAHFCTSIQGLIGSIAGVMATLGYPLPQLP	-----	163		
85	PEARSGSLALDCAPIRLRLGPAPGVSWTAGSPAPAEARTLSRLVKGGSYRKLRRAKQVLE	-----	144		
164	-GTP-----AMADGPAHSDFLQKWDDEWLKELQTWLMRSKADFNRLKKKMQP	-----	211		
145	LGEALIEGCGVGPGEAAVGLQ-----FNLSLSEFSWIRQGE	-----GRILRIRLMP	191		

Search completed: February 9, 2004, 06:15:35
 Job time : 12.5 secs

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DR EMBL, 270692; CA94666.1; ALT_TERM.
 DR EMBL, 270692; CA94665.1; ALT_INIT.
 DR EMBL, AE007074; AAK46576.1; --
 DR TIGR, MT2292; --
 DR Tuberculin; RV2232; --
 DR Tuberculin; RV2233; --
 DR Interpro, IPR005834; Hydrolase.
 DR Pfam, PF00702; Hydrolase; 1.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 291 AA; 30694 MW; 750F090FB154B65 CRC64;
 SQ SEQUENCE

Query Match 6.5%; Score 79; DB 1; Length 291;
 Best Local Similarity 25.8%; Pred. No. 4.6; Matches 65; Indels 54; Gaps 11;
 Matches 47; Conservative 16; Mismatches 65; Indels 54; Gaps 11;

QY 23 PAVPALNRTGDPGPGPSIQKTYDITRYLEHQLSLAGTY---LNYLGPPFNEPDE---- 74
 DB 64 PPAARARASSPGEPSQPL-VIFDLGDTLDSARGIVSPRHNLHICAPVPEGLATHIV 122
 QY 75 NEPRIGAEPLP-----RATVNLVWRSILNDRLRLTQNTYANSHLLCYLR- 118
 DB 123 GPPM--HETLRAMGLGESAEBAIVAYRADYSARGM-----ANMSLFGIGPLADLIRT 173
 QY 119 -GLNQQAATFAR---LRSLAHF-----CRSLGGLGSIAGWATLGYPPLP--P 161
 DB 174 AGVRLAVATSKAEPTARRILRHFGIBQHEVIAGASTDSRGSKVQVLA---HALAQLRP 230
 QY 162 LP 163
 DB 231 LP 232

RESULT 14
 BAT3 HUMAN STANDARD; PRT; 1132 AA.
 ID BAT3_HUMAN
 AC P46379;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Large proline-rich protein BAT3 (HLA-B-associated transcript 3) (G3).
 GN BAT3 OR G3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=90192810; PubMed=2156268;
 RA Banerji J., Sande J., Strominger J.L., Spies T.;
 RT "A gene pair from the human major histocompatibility complex encodes
 RT large proline-rich proteins with multiple repeated motifs and a
 RT single ubiquitin-like domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2374-2378 (1990).
 CC -1- FUNCTION: UNKNOWN.
 CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
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DR EMBL, M33519; AAA35587.1; --
 DR EMBL, M33521; AAA35588.1; --
 DR EMBL, M33520; AAA35588.1; JOINED.
 DR PIR, A35098; A35098.
 DR HSSP, P02248; IUBI.
 DR Genew; HGNC:13919; BAT3.
 DR MIM, 142590; --
 DR GO: GO:0003822; P:MHC-interacting protein; TAS.
 DR Interpro, IPR000626; Ubiquitin.
 DR Pfam, PF00240; Ubiquitin; 1.
 DR SMART, SM00213; UBO; 1.
 DR PROSITE, PS00299; UBIQUITIN_1; 1.
 DR PROSITE, PS00553; UBIQUITIN_2; 1.
 KW Repeat.
 FT DOMAIN 17 77 UBIQUITIN-LIKE.
 FT DOMAIN 202 207 POLY-PRO.
 FT DOMAIN 242 636 4 X 29 AA APPROXIMATE REPEATS.
 FT REPEAT 242 270 1.
 FT REPEAT 415 443 2.
 FT REPEAT 574 602 3.
 FT REPEAT 608 636 4.
 FT REPEAT 657 670 POLY-PRO.
 FT DOMAIN 1132 AA; 119504 MW; E28C8A8A78C38DD18 CRC64;
 SQ SEQUENCE

Query Match 6.5%; Score 79; DB 1; Length 1132;
 Best Local Similarity 26.1%; Pred. No. 26; Matches 67; Indels 46; Gaps 11;
 Matches 46; Conservative 17; Mismatches 67; Indels 46; Gaps 11;

QY 23 PAVPALNRTGDPGPGPSIQKTYDITRYLEHQLSLAGTYLNYLGPPFNEPDEPRLGAE 82
 DB 261 PA-PETNAPNHPSPAEYVEVLQELOR-LESRLQFLOGLYEVNLGAAT-TYNNHDEGRE 317
 QY 83 TLPRATVNLVWRSILNDRLRLTON-YEYSHLLCYLRNQQAAT---AEIRSLAHFPC 137
 DB 318 EDOR-LINL-----VGESLRILGNTFVALSDLRCLN-----ACTPPRHLLHVVRPMSHYT 365
 QY 138 TSLGGLGSIAGWATLGYPPL-----PQPLPGTE-PAMAGPAHS 176
 DB 366 TPM-----VLQQAIPPIQINVTITVTGNGTRPPPPNNAEAPPGFGQASS 412

RESULT 15
 ALK HUMAN STANDARD; PRT; 1620 AA.
 ID ALK_HUMAN
 AC Q9UT73; Q9Y4K6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ALK tyrosine kinase receptor precursor (BC 2.7.1.112) (Anaplastic
 DE lymphoma kinase) (CD246 antigen).
 GN ALK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND
 RP GLYCOSYLATION.
 RX MEDLINE=97316779; PubMed=9174053;
 RA Morris S.W., Naeye C.W., Mathew P., James P.L., Kirstein M.N., Cui X.,
 RA Witte D.P.;
 RT "ALK, the chromosome 2 gene locus altered by the c(2;5) in non-
 RT Hodgkin's lymphoma, encodes a novel neutral receptor tyrosine kinase
 RT that is highly related to leukocyte tyrosine kinase (LTK).";
 RL Oncogene 14:2175-2188 (1997).
 RN (2)
 RN ERRATUM.
 RP Morris S.W., Naeye C.W., Mathew P., James P.L., Kirstein M.N., Cui X.,
 RA Witte D.P.;
 RL Oncogene 15:2883-2883 (1997).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97178863; PubMed=9053841;

GN TCIRG1 OR ATP6N1C.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC TISSUE=Osteoclastoma;
 RX MEDLINE=96158968; PubMed=8579597;
 RA Li Y.P., Chen W., Staehenko P.;
 RT "Molecular cloning and characterization of a putative novel human
 RT osteoclast-specific 116-kDa vacuolar proton pump subunit.";
 RL Biochem. Biophys. Res. Commun. 218:813-821(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RA Busconi L., Delphire E., Robertson E.R., Kojima R., Volk H.D.,
 RA Milford E.L., Guillans S.R.;
 RN Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RX MEDLINE=99263502; PubMed=10329006;
 RA Heilmann T., Bulwin G.C., Randall J., Schnieders B., Sandhoff K.,
 RA Volk H.D., Milford E., Guillans S.R., Utiku N.;
 RT "Genomic organization of the gene coding for TIRG7, a novel membrane
 RT protein essential for T cell activation.";
 RL Genomics 57:398-406(1999).
 CC -1- FUNCTION: PART OF THE PROTON CHANNEL OF V-ATPASES (BY SIMILARITY).
 CC -1- SEEMS TO BE DIRECTLY INVOLVED IN T CELL ACTIVATION.
 CC -1- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
 CC PERIPHERAL CATALYTIC VI COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
 CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
 CC COMPLEX (MAIN COMPONENT: THE PROTOLEPID PROTEIN).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=Q13488-1; Sequence=displayed;
 CC Name=Short;
 CC IsoId=Q13488-2; Sequence=VSP_000345;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: THE LONG ISOFORM IS HIGHLY EXPRESSED IN
 CC OSTEOCLASTOMAS. THE SHORT FORM IS HIGHLY EXPRESSED IN THYMUS.
 CC -1- SIMILARITY: BELONGS TO THE V-ATPASE 116 kDa SUBUNIT FAMILY.
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 CC EMBL: AF030303; AAC31081.2; -
 CC Genew; HGNC:11647; TCIRG1.
 DR MIM: 604592; -
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0005215; P: transporter activity; TAS.
 DR GO: GO:0006968; P: cellular defense response; TAS.
 DR GO: GO:0008284; P: positive regulation of cell proliferation; TAS.
 DR GO: GO:0015992; P: proton transport; TAS.
 DR InterPro: IPR002490; V_ATPase_sub16.
 DR Pfam: PF01966; V_ATPase_sub_a; 1.
 DR Hydrogen ion transport; Transmembrane; Glycoprotein;
 KW Alternative splicing.
 KW DOMAIN 1 397 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 398 418 POTENTIAL.
 FT TRANSMEM 445 465 POTENTIAL.
 FT TRANSMEM 504 524 POTENTIAL.
 FT TRANSMEM 538 558 POTENTIAL.
 FT TRANSMEM 576 596 POTENTIAL.

FT TRANSMEM 636 656 POTENTIAL.
 FT TRANSMEM 771 791 POTENTIAL.
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 503 503 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 216 Missing (in isoform Short).
 FT CONFLICT 377 377 /FTId=VSP_000345.
 FT CONFLICT 603 603 A -> R (IN REF. 1).
 SO SEQUENCE 830 AA; 92997 MW; 62EBAE9A22DC698B CRC64;
 Query Match 6.5%; Score 79.5; DB 1; Length 830;
 Best Local Similarity 24.3%; Pred. No. 16;
 Matches 45; Conservative 25; Mismatches 66; Indels 49; Gaps 9;
 QY 40 IQKTYLTYVLEHQRLSLAGTYLNTVGPFPNEDPRLGATLPRATVNLVWMSLND 99
 DB 61 LEKTP--TFLOEVRV-AGL--VLPPEKGLPAPPR-----D 93
 QY 100 RLRLQNYEAYSHLLCYLRGNRQATATLRSLAFCTSLQGLGSLGVW---ATLGY 156
 DB 94 LRLQETETRLAQELRDVNG-NGQLRLQHLQHLAAVLRQHEPQLAAHTDGSERT 152
 QY 157 PLPQPLPTGEPAMAPQPAHSD---FLQKMDPWLKELQTLWMSAK-----DFNRLKK 207
 DB 153 PLIQ-----ARGGPHQDLRVNFVAGAVPAPKAPALERLLMRACRGFLIASPRELQ 203
 QY 208 KNQPP 212
 DB 204 PLEHP 208
 RESULT 13
 YMS2_MYCTU STANDARD; PRT; 291 AA.
 ID YMS2_MYCTU
 AC Q10515; Q10516;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 26-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein RV2232/RV2233.
 GN RV2232/RV2233 OR MT2292 OR MTCY427.13/MTCY427.14.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagers K., Krogan A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultun J.E., Taylor K., Whitehead S., Barrall B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RX Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Uterback T., Weidman J., Kouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.

RX MEDLINE=91177833; PubMed=2007559;
RA Xu H.W., Wall J.D.;
RT "Clustering of genes necessary for hydrogen oxidation in Rhodobacter
RT capsulatus";
RL J. Bacteriol. 173:2401-2405(1991).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33303 / B10;
RX MEDLINE=93268090; PubMed=8497190;
RA Colbeau A., Richard P., Toussaint B., Caballero F.J., Elster C.,
RA Delphin C., Smith R.U., Chabert J., Vignais P.M.;
RT "Organization of the genes necessary for hydrogenase expression in
RT Rhodobacter capsulatus. Sequence analysis and identification of two
RT hyp regulatory mutants";
RL Mol. Microbiol. 8:15-29(1993).
CC -1- SIMILARITY: BELONGS TO THE HUPK FAMILY.
CC -----
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CC -----
CC EMBL, M55089; AAA72924.1; -
DR EMBL, 215089; CAA78803.1; -
DR PIR, S32947; S32947.
DR CONFLICT 70
SQ SEQUENCE 294 AA; 30222 MW; 2669EB870AF35EDA CRC64;
FT
FT CHAIN 1
FT SIGNAL 22 995
FT CARBOHYD 285 285
FT CARBOHYD 593 593
FT CARBOHYD 625 625
FT CARBOHYD 657 657
FT CARBOHYD 733 733
FT CARBOHYD 793 793
FT CARBOHYD 875 875
FT CARBOHYD 977 977
FT CONFLICT 945
SQ SEQUENCE 995 AA; 114230 MW; 79D21B8CE5A6F62 CRC64;
Query Match 6.6%; Score 84.5; DB 1; Length 294;
Best Local Similarity 31.2%; Pred. No. 1.4; Mismatches 38; Indels 47; Gaps 6;
Matches 40; Conservative 3;
Db 81 LAKLTLWPKLGL-----APQLP---EHMAGGA-----ALQ 111
Qy 76 PERLAETLPRAVNLVWRSINDRLRLTONYEAAYSHLLCYLRGNQATNE---LRRS 132
Db 36 PEGQVALLPR-----LFNLGMAQGHAAIAL-----GLPAEAAPAREILRDH 80
Qy 133 LAHFCTSLGSLGSLAGWATIGYRPLRPLRPTERPMAGRAHSDPFLQMDPFLKLEQ 192
Db 81 LAKLTLWPKLGL-----APQLP---EHMAGGA-----ALQ 111
Qy 193 TWLMSAK 200
Db 112 HWLWGA 119
RESULT 11
MB2_PIG 6.6%; Score 84.5; DB 1; Length 294;
ID MB2_PIG 6.6%; Score 84.5; DB 1; Length 294;
AC Q28949; STANDARD; PRT; 995 AA.
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Epilidymis-specific alpha-mannosidase precursor (EC 3.2.1.24)
DE (Mannosidase alpha class 2B member 2) (AUMAN).
GN MAN2B2.
OS Sue acrota (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Epilidymis;
RX MEDLINE=96117077; PubMed=8562059;
RA Okamura N., Tamba M., Liao H.-D., Once S., Sugita Y., Dacheux F.,
RA Dacheux J.-L.;
RT "Cloning of complementary DNA encoding a 135-kilodalton protein
RT secreted from porcine corpus epididymis and its identification as an
RT epididymis-specific alpha-mannosidase";
RT Mol. Reprod. Dev. 42:141-148(1995).
DE -1- FUNCTION: CAN DIGEST BOTH P-NITRO-PHENYL-ALPHA-D-MANNOSIDE AND

CC HIGH MANNOSIS OLIGOSACCHARIDE (MAN(8)-GLCNAC(2)). MAY BE INVOLVED
CC IN SPERM MATURATION. HAS A POSSIBLE ROLE IN SPECIFIC SPERM-EGG
CC INTERACTION SINCE SPERM SURFACE MANNOSIDASE ACTS LIKE A RECEPTOR
CC FOR MANNOSIS-CONTAINING OLIGOSACCHARIDES LOCATED ON THE ZONA
CC PELLUCIDA.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing alpha-D-
CC mannosidase residues in alpha-D-mannosides.
CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND AT THE SPERM SURFACE AS A
CC 27 kDa FRAGMENT.
CC -1- TISSUE SPECIFICITY: SPECIFIC TO THE CAPUT AND CORPUS OF THE
CC EPIDIDYMIS.
CC -1- PTM: PROCESSED INTO A 27 kDa FRAGMENT LOCALIZED ON THE EQUATORIAL
CC SEGMENT AND THE APICAL RIM OF THE HEAD OF MATURE SPERM.
CC -1- MISCELLANEOUS: OPTIMAL MANNOSIDASE ACTIVITY WAS FOUND AT PH 6.5.
CC -1- SIMILARITY: BELONGS TO FAMILY 38 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@1sb-sdb.ch).
CC -----
CC EMBL, D28521; BAA05877.1; ALT INIT.
DR InterPro: IPR000602; Glyco_hydro_38.
DR Pfam: PF01074; Glyco_hydro_38; 1.
KW Hydrolase; Glycosidase; Signal; Glycoprotein.
FT SIGNAL 1 21
FT CHAIN 22 995
FT CARBOHYD 285 285
FT CARBOHYD 593 593
FT CARBOHYD 625 625
FT CARBOHYD 657 657
FT CARBOHYD 733 733
FT CARBOHYD 793 793
FT CARBOHYD 875 875
FT CARBOHYD 977 977
FT CONFLICT 945
SQ SEQUENCE 995 AA; 114230 MW; 79D21B8CE5A6F62 CRC64;
Query Match 6.6%; Score 80.5; DB 1; Length 995;
Best Local Similarity 23.0%; Pred. No. 16; Mismatches 62; Indels 67; Gaps 9;
Matches 45; Conservative 22;
Db 50 LEHQ---LRSLAGLYNLVLPPEPPNPRLCAETL-----PRATVNLVWRS 97
Db 827 LQHRPVVLFRLIGGVQNGPGRKQEPVTLPPSLILQILSIPTWYSSNHTVHLKMLQK 886
Qy 98 NDR-----LRTONYEAAYSHLLCYLRGNQATNE---LRRS 147
Db 887 HYRRKADPRRVLRLNLHLYENGH---QALSRPT-----LNLQSVLNLGL 929
Qy 148 AGVATLGLYRPLRPLRPTERPMAGRAHSDPFLQMDPFLKLEQTLWMSAKDENR--L 205
Db 930 GSVAVP-----EERSLTGL-----WDVNSLHRMWMKEDGHHNGS 965
Qy 206 KKKQOPP--AASVTLH 219
Db 966 SRRPLRPLRGNVTH 981
RESULT 12
VP3_HUMAN 6.6%; Score 80.5; DB 1; Length 995;
ID VP3_HUMAN 6.6%; Score 80.5; DB 1; Length 995;
AC Q13488; O75877; STANDARD; PRT; 830 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vacuolar proton translocating ATPase 116 kDa subunit A isoform 3 (V-
DE ATPase 116-kDa isoform a3) (Osteoclastic proton pump 116 kDa subunit)
DE (OC-116 kDa) (OC116) (T-cell immune regulator 1) (T cell immune
DE response cDNA) protein) (TIRC7).

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerretti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Shparovski G.V., Uesery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of *Schistosoma* *pombe*.";
 RL Nature 415:871-880(2002)
 CC -1- FUNCTION: BINDS TO AND FACILITATES THE FUNCTIONING OF THE MEIOTIC
 CC REGULATOR MEI2. MAY ALSO BE INVOLVED IN CONJUGATION BY INTERACTING
 CC WITH STE11. ESSENTIAL FOR CELL GROWTH.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Contains 7 WD repeats.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AB032552; BAA84585.1; -
 CC EMBL: Z95396; CAB08769.1; -
 CC PIR: T38943; T38943.
 CC
 CC GeneDB: SPombe; SPAC57A7.1; -
 CC InterPro: IPR001680; WD40.
 CC InterPro: IPR004083; Yeast176.
 CC Pfam: PF00400; WD40; 5.
 CC PRINTS: PR01547; YEAST176DUF.
 CC SMART: SM00320; WD40; 6.
 CC PROSITE: PS00678; WD_REPEATS_1; 1.
 CC PROSITE: PS50882; WD_REPEATS_2; 2.
 CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
 CC Meiosis; WD Repeat; Repeat.
 CC FT REPEAT 986 1029 WD 1.
 CC FT REPEAT 1033 1074 WD 2.
 CC FT REPEAT 1087 1126 WD 3.
 CC FT REPEAT 1130 1170 WD 4.
 CC FT REPEAT 1176 1216 WD 5.
 CC FT REPEAT 1219 1259 WD 6.
 CC FT REPEAT 1268 1308 WD 7.
 CC SO SEQUENCE 1313 AA; 148533 MW; C71B663B0171E7A4 CRC64;
 Query Match 7.0%; Score 86; DB 1; Length 1313;
 Best Local Similarity 22.2%; Pred. No. 7;
 Matches 58; Conservative 31; Mismatches 84; Indels 88; Gaps 12;
 QY 15 LCTVLMHLAV--PALNR-----TGDPGPGSI-----QTYDLTRYLEHQLRS 56
 DB 811 LAFLQHLPALHRAKSLKDTNNSVTSDEPHFVSVSENKILNRSFSLTSKGLALS 870
 QY 57 LAG-----TYANYL-----GPF-FNEBDPFPRLGAEITLPRATNL 91
 DB 871 LAGSRLASLISNGENKPAESNLNHLTSKAVGPPAFNELEQ-----SELDPLTSYIF 926
 QY 92 EVMRSINDRLRLTONYEAYSHLLCYLRG--NRQATAELEKRSIAHPTS-----LOG 142
 DB 927 DMSRKFTPEQKRPNEDEPGSICYNQRLMRNRNKLIRRRPRLAFTSTNGRWNQGLMT 986
 QY 143 LIGSLAGWATLGYPLQPLGTEPAMAGPAHSDPLQKMDDFWLKE--LQTLWLRSA 199
 DB 987 FNNITL-----PRKLMHFQEDQLITLGDKDIQVMDWRN 1022
 QY 200 KDFNRLKKKKQPPASVTLHL 220
 DB 1023 KCLNSFK-----TSASATTNV 1038
 RESULT 9
 PHAC_PSEOL STANDARD; PRT; 560 AA.
 AC P26496;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Poly(3-hydroxyalkanoate) polymerase 2 (EC 2.3.1.-) (PHA polymerase 2)
 DE (PHA synthase 2) (Polyhydroxyalkanoic acid synthase 2).
 GN PHAC.
 OS Pseudomonas oleovorans.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=301;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=GP01.
 RX MEDLINE=91115830; PubMed=1999978;
 RA Huisman G.W., Wontink E., Weima R., Kazemier B., Terpstra P.,
 RA Mitholt B.;
 RT "Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas
 RT oleovorans. Identification and sequences of genes and function of the
 RT encoded proteins in the synthesis and degradation of PHA.";
 RL J. Biol. Chem. 266:2191-2198(1991).
 CC -1- FUNCTION: P.OLEOVORANS ACCUMULATES POLY(3-HYDROXYALKANOATES) AFTER
 CC GROWTH ON MEDIUM CHAIN LENGTH HYDROCARBONS. LARGE AMOUNTS OF THIS
 CC POLYESTER ARE SYNTHESIZED WHEN CELLS ARE GROWN UNDER NITROGEN-
 CC LIMITING CONDITIONS. WHEN NITROGEN IS RESUPPLIED IN THE MEDIUM,
 CC THE ACCUMULATED PHA IS DEGRADED.
 CC -1- SIMILARITY: BELONGS TO THE PHA/PHB SYNTHASE FAMILY.
 CC
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 CC
 CC EMBL: M58445; AAA25934.1; -
 CC PIR: C38604; C38604.
 CC InterPro: IPR000073; A/b hydrolyase.
 CC Pfam: PF00561; abhydrolyase; 1.
 CC KJ PHA biosynthesis; Transferase; Acyltransferase.
 CC FT ACT SITE 296 296 POTENTIAL.
 CC SO SEQUENCE 560 AA; 62631 MW; E2CD844FC1616B83 CRC64;
 Query Match 7.0%; Score 85.5; DB 1; Length 560;
 Best Local Similarity 30.2%; Pred. No. 2.6;
 Matches 38; Conservative 16; Mismatches 43; Indels 29; Gaps 7;
 QY 77 PRLGAEITLPRATVNEVMRSINDRLRLTONYEAYSHLLCYLGLNRQATAELEKRS--A 134
 DB 5 PAKGTPTLPATSMNVQ-----NAIIGLRGR-----DLISTLRNVSROS---LRHPLHTA 50
 QY 135 HFCTSLQGLIGSLAGWATLGYPLQPLG-----TEPAMAGPAHSDPLQKMDDFWLKE 190
 DB 51 HHLALGGQLGRV-----ILGDTPLQPNDRPFRSDPTWSONPFRGLQA---YLAWQ 101
 QY 191 LQTLWLM 196
 DB 102 KQTRLM 107
 RESULT 10
 HUPK_RHOCA STANDARD; PRT; 294 AA.
 ID HUPK_RHOCA
 AC P30757;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hydrogenase expression/formation protein hupK.
 GN HUPK.
 OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 OX NCBI_TaxID=1061;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Fribourg S., Braun I.C., Izaurralde E., Conti E.;
 RT "structural basis for the recognition of a nucleoporin FG repeat by
 RT the NTF2-like domain of the TAP/p15 mRNA nuclear export factor.";
 RL Mol. Cell 8:645-656(2001).
 RP STRUCTURE BY NMR OF 551-619, AND MUTAGENESIS OF PHE-617.
 RX MEDLINE=21912422; PubMed=11875519;
 RA Grant R.P., Hurt E., Neuhaus D., Stewart M.;
 RT "Structure of the C-terminal FG-nucleoporin binding domain of
 RT Tap/Nxf1.";
 RL Nucleic Acids Res. 31:247-251(2003).
 CC -1- FUNCTION: Involved in the nuclear export of mRNA species bearing
 CC retroviral constitutive transport elements (CTE) and in the export
 CC of mRNA from the nucleus to the cytoplasm.
 CC -1- SUBUNIT: Interacts with NXF1, NXF2, E1B-AP5, RAB1, the RRP
 CC proteins and with several nucleoporins.
 CC -1- SUBCELLULAR LOCATION: Nuclear; localized predominantly in the
 CC nucleoplasm and at both the nucleoplasmic and cytoplasmic faces of
 CC the nuclear pore complex. Shuttles between the nucleus and the
 CC cytoplasm.
 CC -1- TISSUE SPECIFICITY: Expressed ubiquitously.
 CC -1- DOMAIN: The minimal CTE binding domain consists of an RNP-
 CC type RNA binding domain (RBD) and leucine-rich repeats.
 CC -1- DOMAIN: The nucleoporin binding domain consists of a NTF2-like
 CC domain and a UBA-like domain. The NTF2 domain heterodimerizes with
 CC NXF1 and NXF2. The formation of NXF1/NXF2 heterodimers is required
 CC for NXF1-mediated nuclear mRNA export. The UBA-like domain
 CC mediates direct interactions with nucleoporin-FG-repeats and is
 CC necessary and sufficient for localization of NXF1 to the nuclear
 CC rim. The conserved loop 594-NMD-596 of the UBA domain has a
 CC critical role in the interaction with nucleoporin.
 CC -1- DOMAIN: The leucine-rich repeats and the NTF2-domain are
 CC essential for the export of mRNA from the nucleus.
 CC -1- MISCELLANEOUS: The RNA-binding domain is a non-canonical RNP-type
 CC domain.
 CC -1- SIMILARITY: BELONGS TO THE NXF FAMILY.
 CC -1- SIMILARITY: Contains 1 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 NTF2 domain.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1- SIMILARITY: Contains 1 UBA-like domain.
 CC -----
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 CC -----
 DR EMBL, AJ133713; CA10753.1; -;
 DR EMBL, AF12880; AAD39102.1; -;
 DR EMBL, AF128246; AAD20016.1; -;
 DR EMBL, BC004904; AAH04904.1; -;
 DR EMBL, AK027192; -; NOT ANNOTATED_CDS.
 DR EMBL, U80073; AAB81111.1; -;
 DR PDB, 1FO1; 03-NOV-00.
 DR PDB, 1FT8; 11-DEC-00.
 DR PDB, 1KOH; 27-FEB-02.
 DR PDB, 1KOO; 27-FEB-02.
 DR PDB, 1OAI; 20-FEB-03.
 DR Genew; HGNC:8071; NXF1.
 DR GK; O9UBU9; -;
 DR MIM; 602647; -;
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003603; LRRcap.
 DR InterPro; IPR002075; NTF2.
 DR InterPro; IPR005637; TAP_C.
 DR PDB; 1GOS; 28-MAR-02.
 DR PDB; 1JUG; 18-DEC-02.
 DR PDB; 1JNS; 23-JUL-01.
 DR Pfam; PF00560; LRR; 1.
 DR Pfam; PF02136; NTF2; 1.
 DR Pfam; PF03943; TAP_C; 1.

DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00446; LRRcap; 1.
 DR PROSITE; PS0177; NTF2 DOMAIN; 1.
 KM Transport; mRNA transport; Nuclear protein; RNA-binding; Repeat;
 FT Leucine-rich repeat; Multigene family; 3D-structure.
 FT DOMAIN 119 198 RNA-BINDING (RRM).
 Query Match 7.0%; Score 86; DB 1; Length 619;
 Best local similarity 25.4%; Pred. No. 2.7;
 Matches 61; Conservative 32; Mismatches 89; Indels 58; Gaps 14;
 QY 5 AGDSWGL-----ACICTVLMHLPAVPALNRTGDP-GRGSIQKTYDLT---RYLEHQL 54
 DB 400 SGRDQGLDAVDHAGCCSLIPFQNPARSLSAEYFQDSRNVKKLKPFTLRLLKQTR 459
 QY 55 RSLACTYINLYGPPNEDRNP--PRGAE--TLPRAVN---LEWMSLNDRLR-LTON 106
 DB 460 LNVV-AFLNEL--PTQHDVNSFVVDISAQSTLLCFSVNGVFKVDKSRDLSLAFRT 516
 QY 107 Y---EAYSHLCTYLRG--LNRQAATAELEKSLAHCSTLSGLGLSISAGVMTLGYLP 161
 DB 517 FIAPVANSGLCTVNDLEFVPMASSEIQKAPF-----MAP 553
 QY 162 LPTGPANAPGPANSDFLQK-----MDFFWLKELQTLW---RSANDFRLKKKQPP 212
 DB 554 TPSSPVPPTLSPEDQEMLQARSTOSGMNLEWSQKCLQNNMDYRSQAQFTLLKAGRI 613
 RESULT 8
 MIPI_SCHPO STANDARD; PRT; 1313 AA.
 ID MIPI_SCHPO
 AC P87141;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE WD-repeat protein mip1.
 GN MIPI OR SPAC57A7.11.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Schizosaccharomycetes; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=20115869; PubMed=10648609;
 RA Shinozaki-Yabana S., Watanabe Y., Yamamoto M.;
 RT "Novel WD-repeat protein Mip1 facilitates function of the meiotic
 RT regulator Mei2p in fission yeast.";
 RL Mol. Cell. Biol. 20:1234-1242(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RX Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hildale J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsle K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voicakert G., Aert R., Roben J., Grymoprez B.,
 RA Wellens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer M., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Weiler H., Wambut R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,

SEQUENCE 1009 AA, 113987 MW, E3DB81DD06135266 CRC64;
Query Match 7.2%; Score 89; DB 1; Length 1009;
Best Local Similarity 23.3%; Pred. No. 3.3;
Matches 45; Conservative 21; Mismatches 65; Indels 62; Gaps 8;
QY 50 LEHQ-----LRSAGTYLNTLVGPPFNEEDFNPRLGATTLPRATVLEWMSLNDRLRLTQ 105
DB 842 LQHRPVVLFGDLAGTAPKLPFGPOQGEAVTLPPNHLQIL-----SIPGMYSSNHTHSQ 896
QY 106 NYRAYSHLCTYAGLNRQAATLRSLAHF-----CTSLQGLGSLAG 149
DB 897 N-----LKKHGEAQAOLRRVLLRLLYHVEVEDPVLISQPTVNLQVLAQLGS 946
QY 150 VMATLGYPLPPLPGTEPAPAPASDFLQKMDFWLKELOTWLRSAKDFNR--LKK 207
DB 947 VVAV-----EERSLTGT-----WDLMLRMKRWKRTGPGHRRDPTTS 982
QY 208 KMGPPAAS-VTLH 219
DB 983 PSRPPGPGPITVH 995
RESULT 7
NXFL HUMAN STANDARD; PRT; 619 AA.
AC 09UBD9; 099799; 09UOL2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nuclear RNA export factor 1 (Tip associating protein) (Tip-associated protein) (mRNA export factor TAP).
OS NXFL OR TAP.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=99219873; PubMed=10202158;
RA Braun I.C., Rohrbach E., Schmitt C., Izaurralde E.;
RT "TAP binds to the constitutive transport element (CTE) through a novel RNA-binding motif that is sufficient to promote CTE-dependent RNA export from the nucleus";
RL EMBO J. 18:1953-1965(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99257272; PubMed=10323864;
RA Kang Y., Cullen B.R.;
RT "The human Tap protein is a nuclear mRNA export factor that contains novel RNA-binding and nucleocytoplasmic transport sequences.";
RL Gene Dev. 13:1126-1139(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99384298; PubMed=10454577;
RA Bear J., Tan W., Zolotukhin A.S., Tabernero C., Hudson E.A., Felber B.K.;
RT "Identification of novel import and export signals of human TAP, the protein that binds to the constitutive transport element of the type D retrovirus mRNA.";
RL Mol. Cell. Biol. 19:6306-6317(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=12477932; PubMed=12477932;
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge C.J., Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Vallilon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., RA Butterfield J.S.N., Krzywicki M.I., Skalska U., Smalls D.E., RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T., RA Yamada K., Fujii Y., Ozaki K., Hideo M., Ohmori Y., Ota T., Suzuki Y., RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., RA Isogai T., Sugano S.;
RT "NEO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE OF 61-619 FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=97318898; PubMed=9175835;
RA Yoon D.-W., Lee H., Seol W., Demaria M., Rosenzweig M., Jung J.U.;
RT "Tap: a novel cellular protein that interacts with tip of herpesvirus salmuri and induces lymphocyte aggregation.";
RL Immunity 6:571-582(1997).
RN [7]
RP FUNCTION.
RX MEDLINE=98325379; PubMed=9660949;
RA Grueter P., Tabernero C., von Kobbe C., Schmitt C., Saavedra C., RA Bachl A., Wilm M., Felber B.K., Izaurralde E.;
RT "TAP, the human homolog of Mex67p, mediates CTE-dependent RNA export from the nucleus";
RL Mol. Cell 1:649-659(1998).
RN [8]
RP CHARACTERIZATION.
RX MEDLINE=21282872; PubMed=11259411;
RA Braun I.C., Herold A., Rode M., Conti E., Izaurralde E.;
RT "Overexpression of rAP15 heterodimers bypasses nuclear retention and stimulates nuclear RNA export";
RL J. Biol. Chem. 276:20536-20543(2001).
RN [9]
RP CHARACTERIZATION.
RX MEDLINE=20132240; PubMed=10668806;
RA Bachl A., Braun I.C., Rodriguez J.P., Pante N., Ribbeck K., RA von Kobbe C., Kutay U., Wilm M., Gorlich D., Carmo-Fonseca M., RA Izaurralde E.;
RT "The C-terminal domain of TAP interacts with the nuclear pore complex and promotes export of specific CTE-bearing RNA substrates.";
RL RNA 6:136-158(2000).
RN [10]
RP MUTAGENESIS.
RX MEDLINE=21151125; PubMed=11256625;
RA Suyama M., Doerks T., Braun I.C., Sattler M., Izaurralde E., Bork P.;
RT "Prediction of structural domains of TAP reveals details of its interaction with p15 and nucleoporins.";
RL EMBO Rep. 1:53-58(2000).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 102-372.
RX MEDLINE=20514125; PubMed=11060011;
RA Liker E., Fernandez E., Izaurralde E., Conti E.;
RT "The structure of the mRNA export factor TAP reveals a cis arrangement of a non-canonical RNP domain and an LRR domain.";
RL EMBO J. 19:5587-5598(2000).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH NXFL, AND X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH NXFL-PG-REPEAT.
RX MEDLINE=21468398; PubMed=11583626;


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RT "Paranodal junction formation and spermatogenesis require
RT sulfoglycolipids";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4227-4232(2002).
CC -I- FUNCTION: Catalyzes the sulfation of membrane glycolipids. Seems
CC to prefer beta-glycosides at the nonreducing termini of sugar
CC chains attached to a lipid moiety. Catalyzes the synthesis of
CC HSO3-3'-galactosylceramide (sulfatide), a major lipid component of
CC the myelin sheath and of HSO3-3'-monogalactosylglycerol
CC (semenolipid), present in spermatozoa. Also acts on
CC lactosylceramide, galactosyl-1-alkyl-2-sn-glycerol and galactosyl
CC diacylglycerol (in vitro).
CC -I- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a
CC galactosylceramide = adenosine 3',5'-bisphosphate +
CC galactosylceramide sulfate.
CC -I- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate +
CC monogalactosylglycerol = adenosine 3',5'-bisphosphate +
CC monogalactosylglycerol sulfate.
CC -I- PATHWAY: Sphingolipid and glycerolipid biosynthesis.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
CC similarity).
CC -I- TISSUE SPECIFICITY: Expressed in brain, testis, kidney, stomach,
CC small intestine, liver, and lung. Not detected in heart, skeletal
CC muscle, and spleen.
CC -I- MISCELLANEOUS: Mice homozygous for a null mutation of the GGT gene
CC display hindlimb weakness from week 6 of age and subsequently show
CC a pronounced tremor and progressive ataxia. Myelin vacuolation is
CC observed in the cerebellar white matter, diencephalon, brainstem
CC and spinal anterior column. Male mice were infertile due to a
CC blocked spermatogenesis.
CC -----
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CC -----
DR DR EMBL, AB032940; BAA93009.1; -
DR EMBL, AB032939; BAA93008.1; -
DR DR EMBL, AK007645; BAB25160.1; -
DR DR EMBL, BC026806; AAB26806.1; -
DR MGD: MG1:1858277; GCst.
DR GO: GO:0016021; C:integral to membrane; IC.
DR GO: GO:0001733; F:galactosylceramide sulfotransferase activity; IDA.
DR GO: GO:0006682; P:galactosylceramide biosynthesis; IDA.
DR GO: GO:0042552; P:myelination; IMP.
DR GO: GO:0007283; P:spermatogenesis; IMP.
KW Transferase; Transmembrane; Glycoprotein.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 35 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT DOMAIN 36 423 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 312 312 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 18 18 L->P (IN REF. 2).
FT CONFLICT 263 263 R->Q (IN REF. 2).
FT CONFLICT 271 271 E->K (IN REF. 2).
FT CONFLICT 358 358 Q->R (IN REF. 1).
FT CONFLICT 392 392 R->G (IN REF. 2).
FT CONFLICT 398 398 I->T (IN REF. 1).
SQ SEQUENCE 423 AA; 48968 MW; FDS4A1A71F4ABE46 CRC64;
Query Match 7.6%; Score 93; DB 1; Length 423;
Best Local Similarity 23.1%; Pred. NO. 0.37;
Matches 55; Conservative 22; Mismatches 65; Indels 96; Gaps 11;
OY 44 YDLTRYLEHQRSLAGTYLVN--LGPP-----FNKP----- 72
DB 204 YDPSSYNAYHLRNLLFPDLGYDSSLDPPASPRVCEHIIEVERRFHVLLOEYFDSESLVLR 263
OY 73 ----DNPNPLGAEITLPRAIVNLFWVRISNDRLRLQNTVEASHL 113

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Db      264  ELUCDDELVDLYYFKLNARSDSPVPLSGELYRAT-----ANNILD--VRLYRHFNASFWR 311
Qy      114  LCIYRLGNLROA-ATNLELRS---LAHFTSLQGLIGSLA-----GWATLGYR 157
Db      318  KVEAFGRERRMAREVAVLROANEHRKHITCIDGQVGVGAIDDSAMQWOPGLIGKSLIGYN 377
Qy      158  LPOPLPGTERPAMAPQPAHSDFLOKDDFWLKEIQ-----TWLMSAKQFN 204
Db      378  LKKS1-----GPOHEQLCRNW-----LPIEIQIYSLDLGALNMLVTKLMLFRDPLR 422

RESULT 4
CTFL_HUMAN
ID CTFL_HUMAN STANDARD, PRT, 201 AA.
AC Q16619,
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardiotrophin-1 (CT-1).
GN CTFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=96429882; PubMed=8830302;
RA Pennica D., Swanson T.A., Shaw K.J., Kuang W.-J., Gray C.L.,
RA Beatty B.G., Wood W.I.;
RT "Human cardiotrophin-1: protein and gene structure, biological and
RT binding activities, and chromosomal localization.";
RL Cycokine 8:183-189(1996).
CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
CC PROSTATE AND OVARY. LOWER LEVELS IN LUNG, KIDNEY, PANCREAS,
CC THYMUS, TESTIS AND SMALL INTESTINE. LITTLE OR NO EXPRESSION IN
CC BRAIN, PLACENTA, LIVER, SPLEEN, COLON OR PERIPHERAL BLOOD
CC LYMPHOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U43033; AAD12173.1; -.
DR EMBL; U43031; AAD12173.1; JOINED.
DR EMBL; U43032; AAD12173.1; JOINED.
DR EMBL; U43030; AAA85229.1; -.
DR PIR; G02312; G02312.
DR Genew; HGNC:2499; CTFL.
DR MIM; 600435; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0005146; F:leukemia inhibitory factor receptor ligand . . .; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007517; P:muscle development; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
KW cytokine; Polymorphism.
FT VARIANTE 92 A -> T (IN dbSNP:2234933) .
FT FT FT /FTID=VAR_014938.
SO SEQUENCE 201 AA; 21227 MW; 0235A7B5745F675F CRC64;
Query Match 7.5%; Score 91.5; DB 1; Length 201;
Best Local Similarity 25.7%; Pctd. No. 0.2;

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Db 84 -SERLR--ODAAALSPALLDVARRRQNELNRPRLRLSLSDAARQVRAALGAAYETVL 140
OY 152 ATIGY-----PLPQPLPCTEPAPAPGPAHSDFLOKXDDDFWLKELQETWLMRSKXDNRL 205
Db 141 AALGAANGPVEPV-ATISALTNSAGVFSKAVLGLHVCGLYGEWWSRTGDLGOL 197

RESULT 2
CTPI_MOUSE STANDARD; PRT; 203 AA.
ID CTPI_MOUSE STANDARD; PRT; 203 AA.
AC 060753;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cardiotrophin-1 (CT-1).
GN CTPI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95166785; PubMed=7862649;
RA Penica D., King K.L., Shaw K.J., Luis E., Rullamae J., Luoh S.-M.,
RA Darbonne W.C., Knutson D.S., Yen R., Chien K.R., Baker J.B.,
RA Wood W.I.;
RT "Expression cloning of cardiotrophin 1, a cytokine that induces
RT cardiac myocyte hypertrophy.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).
CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
CC RECEPTOR/GP 130 RECEPTOR COMPLEX.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
CC LIVER, LUNG AND KIDNEY. LOWER LEVELS IN TESTIS AND BRAIN. NO
CC EXPRESSION IN SPLEN.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC
CC EMBL; U18366; AAC52173.1; .
CC DR PIR; I49153; I49153.
CC DR MGI; MGI:105115; Ctf1.
CC KW Cytokine.
SQ SEQUENCE 203 AA, 21509 MW; 8B3D414A0B3B232F CRC64;

Query Match 9.0%; Score 110.5; DB 1; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.0034;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

OY 40 IOKTDLTRYELHQLRSLAGTYLANTVIGPPRPDPDPRLPPL---GAETLPRAVTLNLEWRS 96
Db 27 IROTNHLALLTKRYAEQLLEBYVOOGGFFGFGPSPLPLAGLSGAPASAGLPV--- 83
OY 97 LNDRLRLTONYEAAYSHLLCYLRLNROA-----TALRLSLAHFCTSLQGLGSIAGVM 151
Db 84 -SERLR--ODAAALSPALLDVARRRQNELNRPRLRLSLSDAARQVRAALGAAYETVL 140
OY 152 ATIGY-----PLPQPLPCTEPAPAPGPAHSDFLOKXDDDFWLKELQETWLMRSKXDNRL 205
Db 141 AALGAANGPVEPV-ATISALTNSAGVFSKAVLGLHVCGLYGEWWSRTGDLGOL 197

RESULT 3
CST_MOUSE STANDARD; PRT; 423 AA.
ID CST_MOUSE STANDARD; PRT; 423 AA.
AC 09JHE4; Q9D8V6;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Galactosylceramide sulfoltransferase (EC 2.8.2.11) (GalCer
DE sulfoltransferase) (Cerebroside sulfoltransferase) (3'-
DE phosphoadenylylsulfate:galactosylceramide 3'-sulfoltransferase)
DE (3'-phosphoadenosine-5'-phosphosulfate:GalCer sulfoltransferase).
GN CST OR GCST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Kidney;
RX MEDLINE=20193614; PubMed=10727929;
RT "cDNA cloning, genomic cloning, and tissue-specific regulation of
RT mouse cerebroside sulfoltransferase.";
RL Eur. J. Biochem. 267:1909-1917(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Ballov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G.,
RA Blake J., Botelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Guestinch S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:665-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kleusner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.B.,
RA Brownstein M.J., Usslin T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION.
RX MEDLINE=21927584; PubMed=11917099;
RA Honke K., Hirahara Y., Dupree J., Suzuki K., Popko B., Fukushima K.,
RA Fukushima J., Nagasawa T., Yoshida N., Wada Y., Taniguchi N.;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2004, 06:14:57 ; Search time 10.5 Seconds

(Without alignments)
1007.715 Million cell updates/sec

Title: US-09-931-704-5

Sequence: 1 MDLRAGDSWGMCLACTVLM.....KKKMPAPASVTLHEAHGF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118.5	9.7	203	CTP1_RAT	Q63086 rattus norv
2	110.5	9.0	203	CTP1_MOUSE	Q60753 mus musculus
3	93	7.6	423	CT1_MOUSE	Q9jhe4 m galactosy
4	91.5	7.5	201	CTP1_HUMAN	Q16619 homo sapien
5	90	7.4	195	CNTF_CHICK	Q02011 gallus gall
6	88	7.2	1009	M2B2_HUMAN	Q9y2es homo sapien
7	86	7.0	619	NKX1_HUMAN	Q9ubn9 homo sapien
8	85.5	7.0	1313	MIPI_SCHPO	P87141 schizosacch
9	85.5	7.0	560	PHAC_PSEOL	P26496 pseudomonas
10	84.5	6.9	294	HUPK_RHOCA	P30797 rhodobacter
11	80.5	6.6	995	M2B2_PIG	Q28649 sus scrofa
12	79.5	6.5	830	VPB3_HUMAN	Q13488 h vacuolar
13	79	6.5	1332	YM32_MYCTU	Q10515 mycobacteri
14	79	6.5	291	YB32_HUMAN	P46379 homo sapien
15	79	6.5	1620	ATKA_HUMAN	Q9um73 homo sapien
16	78.5	6.4	571	ATKA_MYCTU	P96371 mycobacteri
17	78.5	6.4	1473	NAL1_HUMAN	Q9c000 homo sapien
18	78.5	6.4	1844	POLR_TTMV	P10358 turrip yeil
19	78	6.4	422	Y140_HUMAN	Q14153 homo sapien
20	78	6.4	427	RT65_MYXXA	P23071 myxococcus
21	78	6.4	515	YBLJ_SCHPO	Q10340 schizosacch
22	78	6.4	917	SVL_STAUV	P41972 staphylococ
23	77.5	6.3	572	SYM_AERPE	Q9y4y3 aeropyrum p
24	77.5	6.3	1182	HAIR_MOUSE	Q61645 mus musculu
25	77	6.3	2261	RRLP_MUMPM	P30929 mumps virus
26	76.5	6.2	870	BCA1_HUMAN	P56945 homo sapien
27	76.5	6.2	2390	SPCP_HUMAN	Q15020 homo sapien
28	76	6.2	372	CD14_RABIT	Q28680 erythrocyte
29	76	6.2	508	EGRI_RAT	P08154 rattus norv
30	76	6.2	1137	MSB1_YEAST	P21339 saccharomyc
31	75.5	6.2	334	BC12_HUMAN	Q9h009 homo sapien
32	75.5	6.2	346	YG20_YEAST	P53259 saccharomyc
33	75.5	6.2	390	YL28_STRCO	P40181 streptomyce

34	75	6.1	296	1	RECO_ANASP	Q8yD19 anabaena sp
35	75	6.1	343	1	DFRA_SYNY3	P73212 synchocyst
36	75	6.1	452	1	TIL_DROME	P18102 drosophila
37	75	6.1	552	1	MP2_MOUSE	Q9w734 mus musculu
38	75	6.1	715	1	PERB_HUMAN	P15678 homo sapien
39	74.5	6.1	346	1	CNA1_SCHPO	P36599 schizosacch
40	74.5	6.1	1009	1	FAK2_HUMAN	Q14289 h protein t
41	74.5	6.1	1941	1	YRM8_CAEEL	Q09417 caenorhabdi
42	74.5	6.1	2388	1	SPCP_RAT	Q9gwn8 rattus norv
43	74	6.0	388	1	YNJB_BCOLI	P76223 escherichia
44	74	6.0	421	1	PTB2_HUMAN	P49753 homo sapien
45	74	6.0	618	1	NKX1_RAT	Q88984 rattus norv

ALIGNMENTS

RESULT 1	ID	CTP1_RAT	STANDARD	PRT	203 AA.
AC	063086				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	Cardiotrophin-1 (CT-1).				
GN	CTP1.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_Taxid=10116;				
RP	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=WiStar; TISSUE=Heart;				
RA	MEDLINE=96193659; PubMed=8604995;				
RA	Ishikawa M., Saito Y., Miyamoto Y., Kuwahara K., Ogawa E.,				
RA	Nakagawa O., Harada M., Masuda I., Nakao K.;				
RT	"CDNA cloning of rat cardiotrophin-1 (CT-1): augmented expression of				
RT	CT-1 gene in ventricle of genetically hypertensive rats."				
RL	Biochem. Biophys. Res. Commun. 219:377-381(1996).				
CC	- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO				
CC	AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF				
CC	RECEPTOR)/GP 130 RECEPTOR COMPLEX.				
CC	- SUBCELLULAR LOCATION: Secreted (By similarity).				
CC	- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRICLE AND ATRIUM OF ADULT				
CC	RATS. ALSO DETECTED IN THE LUNG, KIDNEY, LIVER, SKELETAL MUSCLE,				
CC	STOMACH AND URINARY BLADDER. NOT DETECTED IN BRAIN, COLON, TESTIS,				
CC	SPLEEN OR THYMUS. OVEREXPRESSED IN THE VENTRICLES IN THE CASE OF				
CC	HYPERTENSION AND HYPERTROPHY.				
CC	- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL, D78591; BAA11427.1; -				
DR	PIR, JC645; JC645.				
KW	Cytokine.				
SO	SEQUENCE 203 AA, 21439 MW, DFB8921A2FA1C832 CRC64;				
QY	Query Match 9.7%; Score 118.5; DB 1; Length 203;				
QY	Best Local Similarity 27.5%; Pred. No. 0.00061;				
QY	Matches 49; Conservative 26; Mismatches 84; Indels 19; Gaps 6;				
DB	40 IOKTDIRRYLEHQRSLAGTYLNTLGPFPNPPNPRL--GAEITPRATVNEFWRS 96				
DB	27 IROTNILARLTQKVAQDLIEVVOQGPFGLGSPRLPLAGLSGAPSPAGLPV--- 83				
QY	97 LNDRLRLQNTVEAYSHLTCYLRGLNRQAA-----TAELRSLAHRCSTSLQGLGSIAGVM 151				

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Qy 61 YNNTGPPN-----EPDFNPRLGATLPRATVNLVWRSINDRLTLTONYEASH 112
Db 71 YLSLKNKLSSGAMRRSQPGVSP---GPE-----TOPEEKRVRELETEQAYVARLH 122
Qy 113 LL--CYLRGLNRQATAELERLSLAHFCTSLQGLGSIAGVMA-TLGYPLPQPLPTEPAW 169
Db 123 LLDQVFFQELREAG-----RSKAPPEVDVKLI FSNISSIYRPHAOFLPE-LQRRVDM 176
Qy 170 ACPAHSDFLQKMDDFWL-----KELOTWLRSAKDFNRLKKKQOPPAASVT 217
Db 177 AATPRIGDVIQKLAAPFLKMYSEYVKNFERAAELATMDKS-QPQEVVTRIQCSAASS 235
Qy 218 LHLEAH 223
Db 236 LTLQHH 241

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Search completed: February 9, 2004, 06:19:06
Job time : 37 secs

DR InterPro; IPR000219; RhGEF.
 DR InterPro; IPR000306; Znf_FYVE.
 DR Pfam; PF01363; FYVE; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00621; RhGEF; 1.
 DR SMART; SM00064; FYVE; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RhGEF; 1.
 DR PROSITE; PS50010; PH_2; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50178; ZF_FYVE; 1.
 SQ SEQUENCE 727 AA; 82099 MW; 5CD0FBFB905C5FC5 CRC64;

Query Match 7.6%; Score 93; DB 11; Length 727;
 Best Local Similarity 24.8%; Pred. No. 3.7;
 Matches 61; Conservative 32; Mismatches 93; Indels 60; Gaps 11;

QY 21 HRPVPAALRTGDPGPGPSIQKTYDLTRYLHQL-----RSLAGT 60
 DB 13 NIVAVFENNRT--PGEAPGSHLEDQPHIPEHQLSLSPPEWAPVYKALKSEFRVPSRT 70
 QY 61 YANYGPPFN-----EPDENPRLGATLPRATVNEVMSLNDRLRLTONYEAH 112
 DB 71 YLSLKNKLSGAMRSCQPGVSP--GPE-----IQEBEKRVRELLETQAVYARLH 122
 QY 113 LH--CYLRGLNRQAATAELRSLAHFCTSLQGLGSIAGVMA-TLGYPLPOLPGTEPAW 169
 DB 123 LLDQVFFQGLAREAG-----RSKAFPEVDVVKLIFSNISSYRHAQFPLP-LQRVNDW 176
 QY 170 APGPAHSDFLQKMDPFWLI-----KELOTWLRSAKDFNRLKKQPPAAV 217
 DB 177 AATPRIGDVIQKLAFLPKMYSEYVKNFERBAELLATWMDKS-QPQEVVTRIQCSBAS 235
 QY 218 LHLFAH 223
 DB 236 LTLQHH 241

RESULT 11

QYBBI PRELIMINARY; PRT; 200 AA.
 AC QYBBI;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein BMET10989.
 GN BMET10989.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=1175668;
 RA Delvecchio V.G., Kapralic V., Redkar R.J., Patra G., Mijer C., Los T.,
 RA Ivanova N., Anderson I., Bhatnagar A., Lykidis A., Renik G.,
 RA Jablonaki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Selkov E., Elser P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyriades N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 RL EMBL; AB09732; AAL54231.1; -.
 DR InterPro; IPR000734; Lipase.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 200 AA; 21513 MW; BAA8596707B67617 CRC64;

Query Match 7.6%; Score 92.5; DB 16; Length 200;
 Best Local Similarity 23.9%; Pred. No. 0.78;
 Matches 55; Conservative 21; Mismatches 89; Indels 65; Gaps 11;

QY 10 GMLACLCTVLMHLPVPAALNRTGDPGPGSIQKTYDLTRYLHQLSLAGTYLNYLGPFF 69
 DB 2 GILAGAAV---LPSPAPAKTQQAAMPNATSPHQADVYL---LRGFADISTGI----- 51
 QY 70 NEPDNPPRLGATLPRATVNEV-----WRLNDRLRLTONYEAHSHLCTLRGLNRQA 124
 DB 52 -----DEIGAE-LQAAGVNAHVQGHAMRLVLRIVADQKNGHLPVLLIGHSLGANA 103
 QY 125 A---TAELRSLAHFCTSLQGLGSIAGVMA-TLGYPLPOLPGT-----EPAW-- 169
 DB 104 ALIYIAEELRR-----GIAVDYMAFPAATGPPPLFGNNRRVYVNFYFKQHGKGL 151
 QY 170 --APGPAHSDFLQKMDPFWLIKELOTWLRSAKDFNRLK-KKQPPAAV 216
 DB 152 PLVPGRRFQHLEND-----FSNAKDVGHFNIEKQRPLOAEV 189

RESULT 12

QYBBI PRELIMINARY; PRT; 232 AA.
 AC QYBBI;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN BRA0258.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Sehnadi R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 RA Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M., Frazer C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014526; AAN33460.1; -.
 DR TIGR; BRA0258; -.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 232 AA; 24810 MW; 612CB963D7A56E18 CRC64;

Query Match 7.6%; Score 92.5; DB 16; Length 232;
 Best Local Similarity 23.9%; Pred. No. 0.95;
 Matches 55; Conservative 21; Mismatches 89; Indels 65; Gaps 11;

QY 10 GMLACLCTVLMHLPVPAALNRTGDPGPGSIQKTYDLTRYLHQLSLAGTYLNYLGPFF 69
 DB 34 GILAGAAV---LPSPAPAKTQQAAMPNATSPHQADVYL---LRGFADISTGI----- 83
 QY 70 NEPDNPPRLGATLPRATVNEV-----WRLNDRLRLTONYEAHSHLCTLRGLNRQA 124
 DB 84 -----DEIGAE-LQAAGVNAHVQGHAMRLVLRIVADQKNGHLPVLLIGHSLGANA 135
 QY 125 A---TAELRSLAHFCTSLQGLGSIAGVMA-TLGYPLPOLPGT-----EPAW-- 169
 DB 136 ALIYIAEELRR-----GIAVDYMAFPAATGPPPLFGNNRRVYVNFYFKQHGKGL 183
 QY 170 --APGPAHSDFLQKMDPFWLIKELOTWLRSAKDFNRLK-KKQPPAAV 216
 DB 152 PLVPGRRFQHLEND-----FSNAKDVGHFNIEKQRPLOAEV 221

RESULT 13

QYBBI PRELIMINARY; PRT; 243 AA.
 AC QYBBI;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN BRA0258.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Sehnadi R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 RA Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M., Frazer C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014526; AAN33460.1; -.
 DR TIGR; BRA0258; -.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 232 AA; 24810 MW; 612CB963D7A56E18 CRC64;

Q8G87 PRELIMINARY: PRT: 8601 AA.
 ID Q8G87
 AC Q8G87
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Mixed type I polyketide synthase/nonribosomal peptide synthetase.
 GN PEDF.
 OS symbiotic bacterium of *Paederus fuscipes*.
 OC Bacteria.
 OX NCBI_TaxID=176282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22294974; PubMed=12381784;
 RA Piel J.;
 RT "A polyketide synthase-peptide synthetase gene cluster from an uncultured bacterial symbiont of *Paederus* beetles";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).
 DR EMBL; AY059471; AAL27851.1;
 SQ SEQUENCE 8601 AA; 948046 MW; C498AC8B086082C7 CRC64;
 Query Match 7.7%; Score 94; DB 2; Length 8601;
 Best Local Similarity 26.1%; Pred. No. 74;
 Matches 52; Conservative 33; Mismatches 72; Indels 42; Gaps 11;
 QY 58 AGTYLNYGPPNPEDPFPRLGAEPLPRATVNLFWMSLNDRLRLTONYEAYSHLGLYL 117
 DB 5078 SGTNHLVVEEVRNSSEDFRLDDVSSSTAPRL-ILSTQDAEKL--EVLNHLAFV 5133
 QY 118 RGLNQAATAELEKSLAHECTSLQG-----LGSINGVATL----- 154
 DB 5134 RQAQNPADLE-RLSLADLAVTLQGRAMEGRVALLVGDLAGLLEALSALREPRCPVS 5192
 QY 155 ---GTPLPQPLPTEPPAPAGPASHDFLQKMDPWL---LKEI-QTWMKSAKQPNRLK 206
 DB 5193 VWSGVVEGPPSGASTVADOPA-AELLQRIPO-WLAEGALDELQAWVAGAPIDMCQR 5250
 QY 207 KKMOPPAASVTLLEAHGF 225
 DB 5251 RR-RPPR---RVHLPSYPP 5265

RESULT 9
 ID 054153 PRELIMINARY: PRT: 640 AA.
 AC 054153
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Transferrase.
 GN SCOS890 OR SC3P7.10.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;
 OC Streptomycetaceae; Streptomycetaceae; Streptomycetaceae;
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8643436;
 RA Redenbach M., Kleier H.M., Denaplatte D., Eichner A., Cullum J.,
 RA Kinoshita H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome";

RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleier H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleier H., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939125; CNA16181.1;
 DR HSSP; P12998; 1850.
 DR InterPro; IPR004839; Aminoacyl-tRNA synthetase/2.
 DR InterPro; IPR006163; PP_bind.
 DR Pfam; PF00155; aminotran_1_2; 1.
 DR Pfam; PF00550; PP-binding; 2.
 DR PROSITE; PS50075; ACP DOMAIN; 1.
 KW Phosphopantetheine; Complete proteome.
 SQ SEQUENCE 640 AA; 68061 MW; E619FB555A613P CRC64;
 Query Match 7.6%; Score 93.5; DB 16; Length 640;
 Best Local Similarity 28.3%; Pred. No. 2.8;
 Matches 52; Conservative 12; Mismatches 63; Indels 57; Gaps 9;
 QY 22 LPAPALNRGDDPGGPGSIQCTYDLTRYLEHQL---RLAGTYLNYGPPNPEDPFPNR 78
 DB 100 LPAPPA-EGTDDPVTBAVAAAMRQYQKHQGLADLEG-----E 140
 QY 79 LGAEPLPRATVNLFWMSLNDRLRLTONYEAYSHLGLYLRLNQAATAELEKSLAHECT 138
 DB 141 LGVDSVLTSSVAE-----TERLGLT-----GAAPDAAGATTLRALA---D 179
 QY 139 SLQGLGSIAGVATLGPPLPQPLPTEPPAPAGPASHDFLQKMDPWLKELQTLWLR 198
 DB 180 ALRGL-----VAAAPGTAPEAAPATGAA-APAGRGSGNAP-----APGADGMDHRS 225

QY 199 AKDF 202
 DB 226 MKDF 229

RESULT 10
 ID 088841 PRELIMINARY: PRT: 727 AA.
 AC 088841
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE FcγRIIb [dysplasia protein 2].
 GN FGD2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9389726; PubMed=10458911;
 RA Pastoris N.G., Gorski J.L.;
 RT "Isolation, characterization, and mapping of the mouse and human fgd2 genes, facitogenital dysplasia (FGD1; aarskog syndrome) gene homologues";
 RL Genomics 50:57-66(1999).
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 DR EMBL; AF017368; AAC35430.1;
 DR MGD; MGI:1347084; Fgd2.
 DR InterPro; IPR001849; PH.

Query Match 11.8%; Score 144.5; DB 13; Length 215;
Best Local Similarity 26.5%; Pred. No. 9.6e-06;
Matches 44; Conservative 34; Mismatches 73; Indels 15; Gaps 4;

QY 56 SLAGTYLNTVIGPPFNPDPNPPRLGAETLPRAATVNLVWRSINDRLRLTQNTYEAYSHLIC 115
DB 55 SLPTFLSFQGAFLSDPDYQLPHIKVNLPTAMADYDFIRQTDETRLKNNLYFYSAIYE 114
QY 116 YLR-----GLN--RQATAELRSLAHFCTSLQGLSIGAVMATLGYPLPGTE 166
DB 115 FLKEAMTEQEDLNPAELALAKAFEEAMANSNT---LISKISIMTQMGMSVITLTP--K 168
QY 167 PAMAPGPASDPLQKMDDFWLKELQTWLRSADKDFNRLKKKQPP 212
DB 169 PLVVPFKGSAYFSKJLRGGVCKEYKERVFLTRKDFMLAEKYQGP 214

RESULT 5
Q9PUJ2 PRELIMINARY; PRT; 215 AA.

AC Q9PUJ2; 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
GN Receptivity factor isoform 1 precursor.
OS Plethodon jordani (Salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
OC Plethodon.
ON NCBI_TaxID=8336;
RN [1]
RX MEDLINE=99420364; PubMed=10489368;
RA Rollman S.M., Houck L.D., Feldhoff R.C.;
RT "Proteinaceous pheromone affecting female receptivity in a terrestrial
salamander";
RL Science 285:1907-1909(1999).
DR EMBL; AF181480; AAF01025.1; -.
KM Signal.
FT SIGNAL. 1 23 POTENTIAL.
SQ SEQUENCE 215 AA; 24138 MW; B1906BB6635738 CRC64;

Query Match 11.8%; Score 144.5; DB 13; Length 215;
Best Local Similarity 25.6%; Pred. No. 9.6e-06;
Matches 41; Conservative 31; Mismatches 81; Indels 7; Gaps 3;

QY 56 SLAGTYLNTVIGPPFNPDPNPPRLGAETLPRAATVNLVWRSINDRLRLTQNTYEAYSHLIC 115
DB 55 SLPTFLSFQGAFLSDPDYQLPHIKVNLPTAMADYDFIRQTDETRLKNNLYFYSAIYE 114
QY 116 YLR-GLNRQ---AATAELRSLAHFCTSLQGLSIGAVMATLGYPLPGTEPAMA 170
DB 115 FLKEAMTEQEDLNPAELALAKAFEEAMANSNTLISKISIMTQMGMSVITLTP--KPLV 172
QY 171 PGPASDPLQKMDDFWLKELQTWLRSADKDFNRLKKKQ 210
DB 173 PREGSAVFRKKJLRGGVCKEYKERVFLTRKDFMLAEKYQGP 212

RESULT 6
Q9PUJ9 PRELIMINARY; PRT; 215 AA.

AC Q9PUJ9; 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
GN Receptivity factor isoform 4 precursor.
OS Plethodon jordani (Salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
OC Plethodon.

OX NCBI_TaxID=8336;
RN [1]
RX MEDLINE=99420364; PubMed=10489368;
RA Rollman S.M., Houck L.D., Feldhoff R.C.;
RT "Proteinaceous pheromone affecting female receptivity in a terrestrial
salamander";
RL Science 285:1907-1909(1999).
DR EMBL; AF181483; AAF01028.1; -.
KM Signal.
FT SIGNAL. 1 23 POTENTIAL.
SQ SEQUENCE 215 AA; 24054 MW; A4A412135FPA4E7F CRC64;

Query Match 11.6%; Score 142.5; DB 13; Length 215;
Best Local Similarity 25.3%; Pred. No. 1.5e-05;
Matches 41; Conservative 33; Mismatches 81; Indels 7; Gaps 3;

QY 56 SLAGTYLNTVIGPPFNPDPNPPRLGAETLPRAATVNLVWRSINDRLRLTQNTYEAYSHLIC 115
DB 55 SLPTFLSFQGAFLSDPDYRLPHIKVNLPTAMADYDFIRQTDETRLKNNLYFYSAIYE 114
QY 116 YLR-GLNRQ---AATAELRSLAHFCTSLQGLSIGAVMATLGYPLPGTEPAMA 170
DB 115 FLKEAMTEQEDLNPAELALAKAFEEAMANSNTLISKISIMTQMGMSVITLTP--KPLV 172
QY 171 PGPASDPLQKMDDFWLKELQTWLRSADKDFNRLKKKQPP 212
DB 173 PFKGSAYFSKJLRGGVCKEYKERVFLTRKDFMLAEKYQGP 214

RESULT 7
Q8N358 PRELIMINARY; PRT; 287 AA.

AC Q8N358; 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
GN Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RX MEDLINE=99420364; PubMed=10489368;
RA Rollman S.M., Houck L.D., Feldhoff R.C.;
RT "Proteinaceous pheromone affecting female receptivity in a terrestrial
salamander";
RL Science 285:1907-1909(1999).
DR EMBL; AF181483; AAF01028.1; -.
KM Signal.
FT SIGNAL. 1 23 POTENTIAL.
SQ SEQUENCE 287 AA; 32156 MW; 6E571BCA0328E74E CRC64;

Query Match 7.7%; Score 94; DB 4; Length 287;
Best Local Similarity 22.3%; Pred. No. 0.9;
Matches 47; Conservative 18; Mismatches 62; Indels 84; Gaps 9;

QY 15 LCTVIMHLPAVVALNRITGPGGPGPSIQTYD-----LTRY---LEHQL--RSLAG 59
DB 132 LPLVWLRP-----PDGPPTLNTLQCPGSRQSPGVLRRHNOIMHVLTGGAFTN 181
QY 60 TYLNTY-----LGPFPNPDPNPPRLGAETLPRAATVNLVWRSINDRLRLTQNTYEAYSHLIC 115
DB 182 TYLFGAIVRGV-----PDGPPTLNTLQCPGSRQSPGVLRRHNOIMHVLTGGAFTN 204
QY 116 YLRGLNRQAAATAEELRSLAHFCTSLQGLSIGA-----GVNATLGYPLPGTEPAMA 169
DB 205 YL-----LSPLACLILCFGTLHQLLSTLASPGAGGPAAPAHWPACPLPGIPLRLO 256
QY 170 ACPASDPLQKMDDFWLKELQTWLRSADKDFNRLKKKQPP 212
DB 257 LPPPHAAVLRAGAAGMDYWRGSRFLPMPGW 287

RESULT 8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2004, 06:14:57 ; Search time 36 Seconds

(without alignments)
1612.823 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224

Sequence: 1 MDLRAGDSWGMCLACTVLM.....KKMKPPASVTLHLRNGF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertedrate:*

14: sp_unclassified:*

15: sp_rv1rus:*

16: sp_bacteriapi:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	100.0	225	11	Q9QZM3
2	1193	97.5	225	4	Q9UBD9
3	144.5	11.8	215	13	Q9PUJ1
4	144.5	11.8	215	13	Q9PUJ0
5	144.5	11.8	215	13	Q9PUJ2
6	142.5	11.6	215	13	Q9PUJ9
7	94	7.7	287	4	Q8N358
8	94	7.7	8601	2	Q8GM87
9	93.5	7.6	640	16	Q54153
10	93	7.6	727	11	Q88841
11	92.5	7.6	200	16	Q8YB81
12	92.5	7.6	232	16	Q8FX31
13	92.5	7.6	243	10	Q8NEV9
14	92	7.5	332	10	Q9MAU1
15	92	7.5	655	11	Q8BY35
16	91.5	7.5	455	11	Q9CWM7

17	90	7.4	733	16	Q9HTC5	Q9htc5 pseudomonas
18	89.5	7.3	379	2	Q8KRX4	Q8kxr4 streptomyces
19	89.5	7.3	530	3	Q8XOE9	Q8xoe9 neuropeptide
20	89	7.3	733	16	Q91664	Q91664 pseudomonas
21	88	7.2	222	2	Q91584	Q91584 streptococcus
22	87	7.1	332	2	Q8KNP2	Q8knp2 streptococcus
23	86.5	7.1	318	4	Q96152	Q96152 homo sapiens
24	85.5	7.0	389	17	Q9YA71	Q9ya71 aeropyrum p
25	85.5	7.0	522	7	Q8HWH4	Q8hwh4 mus musculus
26	85.5	7.0	1122	10	Q8GVC8	Q8gvc8 oryza sativa
27	85.5	7.0	1154	11	Q921R2	Q921r2 mus musculus
28	85	6.9	332	11	Q8B113	Q8b113 mus musculus
29	85	6.9	422	11	Q8BGR5	Q8bgr5 mus musculus
30	85	6.9	476	11	Q8R363	Q8r363 mus musculus
31	85	6.9	520	16	Q9RT14	Q9rt14 deinosoccus
32	85	6.9	585	5	Q9VNR6	Q9vnr6 drosophila
33	85	6.9	1024	16	Q8FRH1	Q8frh1 corynebacter
34	84.5	6.9	716	16	Q8PT99	Q8pt99 xanthomonas
35	84	6.9	468	16	Q8DHQ5	Q8dhq5 synchococcus
36	84	6.9	741	16	Q9H2M0	Q9h2m0 pseudomonas
37	83	6.8	272	16	Q86721	Q86721 streptomyces
38	83	6.8	396	2	Q9AR00	Q9arf0 frankia sp.
39	83	6.8	456	13	Q8AYL4	Q8ayl4 oncorhynchus
40	83	6.8	955	11	Q88287	Q88287 mus musculus
41	83	6.8	1561	11	Q88286	Q88286 mus musculus
42	82.5	6.7	213	2	Q8GNS7	Q8gns7 streptococcus
43	82.5	6.7	1098	11	Q9WTN8	Q9wtn8 rattus norvegicus
44	82.5	6.7	5990	2	Q9RLP6	Q9rlp6 mycobacterium
45	81.5	6.7	209	2	Q91593	Q91593 streptococcus

ALIGNMENTS

RESULT 1	ID	Q9QZM3	PRELIMINARY	PRT	225 AA.
AC	Q9QZM3				
DT	01-MAY-2000	(TREMBLrel. 13, Created)			
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)			
DE	Neurotrophin-1/B-cell stimulating factor-3.				
GN	BSF3.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxId=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99432254; PubMed=10500198;				
RA	Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,				
RA	Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Mann F.,				
RA	Simonet W.S., Boone T., Chang M.-S.,				
RT	"Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the				
RT	IL-6 family."				
RT	Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463 (1999).				
DR	EMBL, AF176913; AAF00993.1; -				
DR	MED, MGI:1930088; Bsf3.				
SQ	SEQUENCE 225 AA; 25261 MW; 68B1FEAAB7F1A950 CRC64;				
Query Match	100.0%; Score 1224; DB 11; Length 225;				
Best Local Similarity	100.0%; Pred. No. 1.8e-108;				
Matches	225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 MDLRAGDSWGMCLACTVLMHLPALNRTGDPGSPSIQKTYDLTRYLHQLRLSLACT 60				
DB	1 MDLRAGDSWGMCLACTVLMHLPALNRTGDPGSPSIQKTYDLTRYLHQLRLSLACT 60				
QY	61 YANYIGPPNEDPDPNPRGATTPRAYTNLEWMSINDRLALNTQYEAYSHLCTRL 120				
DB	61 YANYIGPPNEDPDPNPRGATTPRAYTNLEWMSINDRLALNTQYEAYSHLCTRL 120				
QY	121 NQGAATFALRLSRSLAFHCTSLGGLGSLAGVMTLGLPLPGLPTEPAAPAPASDPLQ 180				

Query Match 95.7%; Score 1171; DB 22; Length 321;
 Best Local Similarity 96.0%; Pred. No. 1.9e-115;
 Matches 214; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 LRAGSWGMLACTVLMHLPVAPALNRGDPGPGSIQKTYDLTRYLEHQLRSIAGTYL 62
 DB 99 LFTGSWGMALACTVLMHLPVAPALNRGDPGPGSIQKTYDLTRYLEHQLRSIAGTYL 158
 QY 63 NYLGPPNEPDNPRLGAETLPRAVTNLEWVRSINDRLRLTONYEAVSHLLCYLRGLNR 122
 DB 159 NYLGPPNEPDNPRLGAETLPRAVTNLEWVRSINDRLRLTONYEAVSHLLCYLRGLNR 218
 QY 123 QATATLRRSLAHFCTSLQGLLSIAGVMAATLGYPLPOPLPCTEPAMADGPAHSDFLQKM 182
 DB 219 QATATLRRSLAHFCTSLQGLLSIAGVMAATLGYPLPOPLPCTEPAMADGPAHSDFLQKM 278
 QY 163 DDFWLLKEIQTWLMRSKDFNRLKKMOPPAASVTLHLEAHGF 225
 DB 279 DDFWLLKEIQTWLMRSKDFNRLKKMOPPAASVTLHLEAHGF 321

RESULT 15
 AAB19587
 ID AAB19587 standard; Protein; 215 AA.
 AC AAB19587;
 XX 22-JAN-2001 (first entry)
 DT Mouse Interleukin-B60 (IL-B60).
 DE Interleukin-B60; IL-B60; mouse; cytokine; cytokine-like factor-1;
 KW haematopoietic; inflammation; antiinflammatory; autoimmune disease;
 KM therapy.
 OS Mus musculus.
 XX Key Location/Qualifiers
 FH 1..17
 FT Peptide /label= Signal_peptide
 FT Protein /label= Mature-protein
 PN WO200053631-A1.
 PD 14-SEP-2000.
 PF 09-MAR-2000; 2000WO-US06182.
 PR 11-MAR-1999; 99US-0267901.
 PA (SCHE) SCHERING CORP.
 PI Oppmann B, Tjamae JC, Kastelein RA, Bazan JF;
 DR WPI; 2000-587426/55.
 DR N-PSDB; AAB88547.
 XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
 PT polypeptides, and nucleic acids, useful in research, diagnosis and for
 XX treating inflammatory and autoimmune disorders -
 PS Claim 1; Page 17; 97pp; English.

The present sequence is that of mouse interleukin-B60 (IL-B60), a novel, small soluble cytokine-like protein that exhibits structural motifs characteristic of a member of the long-chain cytokines, and which shows homology to granulocyte colony stimulating factor and interleukin-6. IL-608 may have either stimulatory or inhibitory effects on haematopoietic cells, including e.g. lymphoid cells, such as T-cells, B-cells, natural killer cells, macrophages, dendritic cells, haematopoietic progenitors, etc. Methods are provided for modulating the physiology or development of a cell or

CC tissue culture cells by contacting the cell with an agonist or
 CC antagonist of IL-B60 or an agonist of antagonist of a complex of
 CC mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see
 CC AAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological
 CC factor in motor neuron development and regeneration. IL-608, its
 CC agonists and antagonists may be used to treat inflammatory or
 CC autoimmune disorders and also for drug screening.
 XX

SQ Sequence 215 AA;
 Query Match 95.3%; Score 1167; DB 21; Length 215;
 Best Local Similarity 100.0%; Pred. No. 2.9e-115;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MIACTCTVLMHLPVAPALNRGDPGPGSIQKTYDLTRYLEHQLRSIAGTYLNYLGPPN 70
 DB 1 MIACTCTVLMHLPVAPALNRGDPGPGSIQKTYDLTRYLEHQLRSIAGTYLNYLGPPN 60
 QY 71 EPDFNPRLGAETLPRAVTNLEWVRSINDRLRLTONYEAVSHLLCYLRGLNRQAATAELR 130
 DB 61 EPDFNPRLGAETLPRAVTNLEWVRSINDRLRLTONYEAVSHLLCYLRGLNRQAATAELR 120
 QY 131 RSLAHFCTSLQGLLSIAGVMAATLGYPLPOPLPCTEPAMADGPAHSDFLQKMDFWLLKE 190
 DB 121 RSLAHFCTSLQGLLSIAGVMAATLGYPLPOPLPCTEPAMADGPAHSDFLQKMDFWLLKE 180
 QY 191 LOTWLMRSKDFNRLKKMOPPAASVTLHLEAHGF 225
 DB 181 LOTWLMRSKDFNRLKKMOPPAASVTLHLEAHGF 215

Search completed: February 9, 2004, 06:16:54
 Job time : 35.5 secs

PN WO200157188-A2.
 XX 09-AUG-2001.
 PD 05-FEB-2001; 2001WO-US03800.
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-457740/49.
 DR N-PSDB; ABA09140.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX
 XX Claim 20; Page 273; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB1230 represent 1350 novel human polypeptides, and
 CC sequences ABA08223-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, hematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.
 CC
 CC Sequence 321 AA;
 XX
 SQ

QY 123 QATATLRRSLAHFCTSLQGLGSIAGWATLGYPLPQPLPTEBPAMAPPAHSDFLQRM 182
 DB 219 QATATLRRSLAHFCTSLQGLGSIAGWAAALGYPLPQPLPTEBPMTWTPGPHSDFLQRM 278
 QY 183 DDFWLKELQTLWLRSAKDPPNRLKKKMPAASVTLHLEAHGF 225
 DB 279 DDFWLKELQTLWLRSAKDPPNRLKKKMPAASVTLHLEAHGF 321
 RESULT 14
 AAM79399
 ID AAM79399 standard; Protein; 321 AA.
 AC AAM79399;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3045.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZM;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 DR WPI; 2001-476283/51.
 DR N-PSDB; AAK52532.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 237; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAK80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 CC
 CC Sequence 321 AA;
 XX
 SQ

CC cells they are expressed in, such as: antiinflammatory; antineumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianemic; antilagregant; haemostatic; vulnery;
CC antidiabetic; osteopathic; dermatological; antiallergic; antiaesthetic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.

SQ Sequence 253 AA;

Query Match 97.5%; Score 1193; DB 22; Length 253;
Best Local Similarity 96.9%; Pred. No. 6.3e-118;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACICTVLMHLPVAVPALNRGDPGPGPSIOKTYDITRYLEHQRLSLAGT 60
DB 29 MDLRAGDSWGMACICTVLMHLPVAVPALNRGDPGPGPSIOKTYDITRYLEHQRLSLAGT 88
QY 61 YLNTYGPPNPEDFPNPRPGAETLPRAVTNLEWRSNDRLRLTONYEAYSHLLCYLRGL 120
DB 89 YLNTYGPPNPEDFPNPRPGAETLPRAVTNLEWRSNDRLRLTONYEAYSHLLCYLRGL 148
QY 121 NROAATAEIRSLAFCTSLGGLGSLAGVWATLGYPLPGTEPPMAGPASHDFLQ 180
DB 149 NROAATAEIRSLAFCTSLGGLGSLAGVWATLGYPLPGTEPPMAGPASHDFLQ 208
QY 181 KMDDFWLKEQLQTLWMSAKDFNRLKKMQPPAASVTTLHLGAHF 225
DB 209 KMDDFWLKEQLQTLWMSAKDFNRLKKMQPPAASVTTLHLGAHF 253

RESULT 12

AAE00828
ID AAE00828 standard; Protein; 223 AA.

AC AAE00828;

DT 02-JUL-2001 (first entry)

DE Human cardiotrophin-like cytokine (CLC) protein.

KM Human; biologically active complex; haemopoietin receptor; NR6;
KM cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
KM differentiation; cell survival; neurotrophic activity.

OS Homo sapiens.

XX Key Location/Qualifiers
XX Peptide 1..27
XX PT /label= Signal_peptide
XX PT 28..223
XX PT /label= Human_mature_CLC_protein
XX PT /note= "Cardiotrophin-like cytokine"

WO200127157-A1.

19-APR-2001.

06-OCT-2000; 2000WO-AU01216.

08-OCT-1999; 99AU-0003327.

PR 12-MAY-2000; 2000AU-0007489.

XX (AMRA) AMRAD OPERATIONS PTY LTD.

PI Naah A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;

PI Nakata Y, Hasegawa M;

DR WPI; 2001-281978/29.

DR N-PSDB; AAD04201.

PT New biologically active complex comprising NR6 and

PT cardiotrophin-like-cytokine, for facilitating proliferation,

CC differentiation and/or survival of a cell -

CC Claim 32; Page 114-115; 123pp; English.

CC The present invention relates to a biologically active complex comprising

CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC).

CC The complex is useful in the manufacture of a medicament for the

CC treatment and/or prophylaxis of a subject, as it is involved in

CC facilitating proliferation, differentiation and/or survival of a cell.

CC The complex or its components have neurotrophic activity. The present

CC sequence is human cardiotrophin-like cytokine (CLC) protein.

SQ Sequence 223 AA;

Query Match 96.5%; Score 1181; DB 22; Length 223;
Best Local Similarity 96.9%; Pred. No. 9.8e-117;
Matches 216; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACICTVLMHLPVAVPALNRGDPGPGPSIOKTYDITRYLEHQRLSLAGT 60
DB 1 MDLRAGDSWGMACICTVLMHLPVAVPALNRGDPGPGPSIOKTYDITRYLEHQRLSLAGT 60
QY 61 YLNTYGPPNPEDFPNPRPGAETLPRAVTNLEWRSNDRLRLTONYEAYSHLLCYLRGL 120
DB 61 YLNTYGPPNPEDFPNPRPGAETLPRAVTNLEWRSNDRLRLTONYEAYSHLLCYLRGL 120
QY 121 NROAATAEIRSLAFCTSLGGLGSLAGVWATLGYPLPGTEPPMAGPASHDFLQ 180
DB 121 NROAATAEIRSLAFCTSLGGLGSLAGVWATLGYPLPGTEPPMAGPASHDFLQ 180
QY 181 KMDDFWLKEQLQTLWMSAKDFNRLKKMQPPAASVTTLHLGAH 223
DB 181 KMDDFWLKEQLQTLWMSAKDFNRLKKMQPPAASVTTLHLGAH 223

RESULT 13

ABBI1896
ID ABBI1896 standard; peptide; 321 AA.

AC ABBI1896;

DT 11-JAN-2002 (first entry)

DE Human cardiotrophin-like cytokine homologue, SEQ ID NO:2266.

KM Human; cytokine; cell proliferation; cell differentiation; growth factor;
KM haematopoiesis regulation; tissue growth; immunomodulator; activin;
KM inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KM proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KM chronic inflammatory condition; proliferative retinopathy;
KM atherosclerosis; coronary heart disease; arterial lechaemia;
KM bone disorder; osteoporosis; vascular growth disorder;
KM tissue regeneration; wound healing; infection; immune disorder;
KM cell culture; drug screening; gene therapy; antiinflammatory;
KM antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KM cyostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KM antifungal; vulnery; antidiabetic.

OS Homo sapiens.

RESULT 10
AAU78176
ID AAU78176 standard; Protein; 225 AA.
XX AC AAU78176;
XX 05-JUN-2002 (first entry)
XX Human novel neurotrophic factor NNT1.
DE Human novel neurotrophic factor NNT1.
XX
XX Human; NNT1; neurotrophic factor; IGF-related disease;
XX Type I allergic disease; allergic rhinitis; eczema; dermatitis;
XX pollinosis; asthma; immune disease; cancer; arteriosclerosis;
XX vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
XX inflammatory arthritis; osteoarthritis; inflammatory joint disease;
XX autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
XX inflammatory bowel disease; transplant rejection; reproductive disorder;
XX graft versus host disease; infertility; miscarriage; preterm labour.
XX
XX Homo sapiens.
XX WO200215977-A2.
XX 28-FEB-2002.
XX 17-AUG-2001; 2001WO-US25906.
XX 18-AUG-2000; 2000US-226436P.
XX 16-AUG-2001; 2001US-0931704.
XX (AMGE-) AMGEN INC.
XX Senaldi G;
XX WPI; 2002-280867/32.
XX N-PSDB; ABK11647.
XX
XX Treating Immunoglobulin E-related disease, modulating IGE levels in a
XX patient, preventing IGE-related disease and treating allergic diseases,
XX involves administering NNT-1 inhibitor to a patient
XX
XX Claim 2; Fig 3; 63pp; English.
XX
XX The invention relates to treating Immunoglobulin E (IGE)-related disease,
XX modulating IGE levels in a patient, preventing an IGE-related disease,
XX and treating allergic diseases, comprising administering a
XX therapeutically effective amount of novel neurotrophic factor (NNT)-1
XX inhibitor to a patient. Also included are a method of diagnosing an
XX IGE-related disease or susceptibility to an IGE-related disease, by
XX determining the presence or amount of expression of an NNT1 polypeptide
XX encoded by a NNT1 nucleotide sequence, its fragment or naturally
XX occurring variant, and diagnosing an IGE-related disease or
XX susceptibility of an IGE-related disease based on the presence or amount
XX of expression of the polypeptide and a pharmaceutical composition for use
XX in treating IGE-related disease, comprising the NNT1 inhibitor.
XX The NNT1 inhibitor is useful for preventing and treating IGE-related
XX disease, modulating IGE levels, and treating allergic diseases e.g.
XX Type I allergic disease, allergic rhinitis, eczema, dermatitis,
XX pollinosis, asthma, immune diseases and disorders, diseases involving
XX abnormal cell proliferation including cancer, arteriosclerosis and
XX vascular restenosis, diseases and conditions relating to dysfunction of
XX immune system including rheumatoid arthritis, psoriatic arthritis,
XX inflammatory arthritis, osteoarthritis, inflammatory joint disease,
XX autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
XX bowel disease, transplant rejection, and graft versus host disease, and
XX reproductive diseases and disorders including infertility, miscarriage,
XX preterm labour and delivery, and endometriosis. The present sequence
XX represents human NNT1.
XX
XX Sequence 225 AA;

Query Match 97.5%; Score 1193; DB 23; Length 225;
Best Local Similarity 96.9%; Pred. No. 5.3e-118;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDLRAGDSWGMALACTIVMHLPAVPALNRGTGDPGPGPSIQKTYDITRYLEHQLRLSLAGT 60
DB 1 MDLRAGDSWGMALACTIVMHLPAVPALNRGTGDPGPGPSIQKTYDITRYLEHQLRLSLAGT 60
QY 61 YLNYLGPFPNEPDPNPRIGAEITLPPATVNLLEWRSLSNRLRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYLGPFPNEPDPNPRIGAEITLPPATVNLLEWRSLSNRLRLTONYEAYSHLLCYLRGL 120
QY 121 NRQATATAEILRRSLAHPCTSLQGLGSIAGVMAITLGYPLPOPLGTEPPAPAPGPHSDPLQ 180
DB 121 NRQATATAEILRRSLAHPCTSLQGLGSIAGVMAITLGYPLPOPLGTEPPAPAPGPHSDPLQ 180
QY 181 KMDDFWLKELQTMWRSKADNRRLKKKQPPAASVTLHLGAHGF 225
DB 181 KMDDFWLKELQTMWRSKADNRRLKKKQPPAASVTLHLGAHGF 225
RESULT 11
AAM25831
ID AAM25831 standard; Protein; 253 AA.
XX AC AAM25831;
XX 16-OCT-2001 (first entry)
XX Human protein sequence SEQ ID NO:1346.
XX
XX Human; cancer; HIV infection; human immunodeficiency virus;
XX antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
XX antibacterial; endocrine; cardiac; central nervous system; vitamin;
XX anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
XX antiaggregant; haemostatic; vulnery; antitumor; osteopathic; eczema;
XX dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
XX neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
XX immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
XX antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
XX cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
XX genetic disease; haematopoietic disorder; platelet disorder; asthma;
XX thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
XX allergic rhinitis; diabetes; multiple sclerosis; depression;
XX Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
XX neurological disorder.
XX
XX Homo sapiens.
XX WO200153455-A2.
XX 26-JUL-2001.
XX 22-DEC-2000; 2000WO-US35017.
XX 23-DEC-1999; 99US-0471275.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457603/49.
XX N-PSDB; AAH99772.
XX Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX Claim 20; Page 278; 1217pp; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
XX AAM25963. The proteins can have activities based on the tissues and

PR 03-FEB-1997; 97US-0792019.
 XX (AMGE-) AMGEN INC.
 PA Chang M,
 PI
 XX MPI; 2000-338492/29.
 DR N-PSDB; AAA39481.
 XX
 PT New nucleic acids encoding neurotrophic factors useful for stimulating
 PT growth of motor or sympathetic neurons for treating neuron cell damage
 PS
 XX
 PS Claim 1c; Fig 3; 42pp; English.
 XX
 CC This invention describes a novel nucleic acid molecule (i) encoding a
 CC novel neurotrophic factor (NNT-1) (ii) which has neurotrophic,
 CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
 CC ophthalmological activity. (i) is useful for producing NNT-1
 CC polypeptides which are useful for treating patients in whom various
 CC cells of the central, autonomic, or peripheral nervous system have
 CC degenerated and/or have been damaged by congenital disease, trauma,
 CC mechanical damage, surgery, stroke, ischemia, infection, metabolic
 CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
 CC proteins are used to treat diseases like Alzheimer's, Parkinson's,
 CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
 CC disease, peripheral neuropathy induced by diabetes or other metabolic
 CC disorders, and/or dystrophies or degeneration of the neural retina such
 CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
 CC night blindness, progressive cone-rod degeneration, immune disorders and
 CC hematopoietic disorders. (i) is effective in treating neurological
 CC conditions and promotes neuron regeneration. Neural functions are
 CC effectively restored in patients suffering from various neurological
 CC disorders. This sequence represents the human NNT-1 protein described in
 CC the method of the invention.
 CC
 SQ Sequence 225 AA;
 Query Match 97.5%; Score 1193; DB 21; Length 225;
 Best Local Similarity 96.9%; Pred. No. 5.3e-118;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

KW muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
 KW blastocyst implantation; thrombosis; retinal disease;
 KW retinal pigmentosis.
 XX
 XX Homo sapiens.
 OS
 XX MO200155172-A2.
 PN
 XX
 XX 02-AUG-2001.
 PD
 XX
 XX 26-JAN-2001; 2001WO-FR00253.
 PF
 XX 27-JAN-2000; 2000FR-0001035.
 PR 12-OCT-2000; 2000FR-0013089.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI
 XX Elson G, Gauchat J, Plun-Favreau H, Chevallier S, Gascan H;
 DR MPI; 2001-488773/53.
 DR N-PSDB; AAH74484.
 PT
 PT A complex comprising a NNT-1 protein and a CLF-1 and/or scNTRalpha
 PT protein useful to treat neurodegenerative disease including Parkinson's
 PT and Huntington's, obesity and cancer
 PS
 PS Claim 2; Page 58; 67pp; French.
 XX
 XX The present sequence represents a human NNT-1 protein. The specification
 XX describes a complex comprising a NNT-1 protein and a CLF-1 and/or
 XX scNTRalpha protein. The NNT-1/CLF-1 complex is used to modulate
 XX activity of the scNTRalpha/gp130/LIFRbeta receptor complex, or to
 XX induce phosphorylation of the tyrosine of gp130 and LIFRbeta,
 XX particularly where cells expressing the receptor complex are in the
 XX central or peripheral nervous system, in neurons implicated in
 XX neuro-muscular function or in skeletal muscle. The complex or
 XX antibodies are also used to decrease the survival, growth or
 XX proliferation of tumour cells or to facilitate the proliferation and/or
 XX inhibit differentiation of cells stocks. The complex is also used to
 XX modulate activity of the gp130/LIFRbeta receptor or cells expressing
 XX that receptor, particularly those cells implicated in the immune,
 XX haematopoietic, nervous or reproductive system, the liver or skeletal
 XX muscle. Molecules of the invention may be used to prevent or treat
 XX neurodegenerative diseases including amyotrophic lateral sclerosis,
 XX Parkinson's and Huntington's disease, to repair or regenerate nervous
 XX or muscular tissue or to maintain muscular mass in paralysis patients.
 XX They may also be used to treat cancer, obesity and associated diseases,
 XX and to improve fertility, particularly to avoid endometriosis and/or
 XX assist blastocyst implantation, thrombosis, or retinal disease,
 XX particular retinal pigmentosis.
 SQ Sequence 225 AA;
 Query Match 97.5%; Score 1193; DB 22; Length 225;
 Best Local Similarity 96.9%; Pred. No. 5.3e-118;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

XX PS Claim 1; Fig 3; 41pp; English.
XX CC The present sequence represents a human neurotrophic factor, designated
XX CC NNT-1, which is capable of stimulating growth of motor or sympathetic
XX CC neurons. The NNT-1 protein is useful in the treatment of neurological
XX CC diseases characterised by the degeneration and death of particular
XX CC classes of neurons. These diseases specifically include Parkinson's
XX CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
XX CC stroke and various degenerative disorders affecting vision.
SQ Sequence 225 AA:

Query Match 97.5%; Score 1193; DB 19; Length 225;
Best Local Similarity 96.9%; Pred. No. 5.3e-118;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACLTCTVLMHLPAPALNRTGDPGPGPSIQKTYDITRYLEHQLSLAGT 60
DB 1 MDLRAGDSWGMACLTCTVLMHLPAPALNRTGDPGPGPSIQKTYDITRYLEHQLSLAGT 60
QY 61 YNLYGPPNEPDPNPRLGAETLPRAVTNLEWRSLSNDRRLTONYEAYSHLLCYLRGL 120
DB 61 YNLYGPPNEPDPNPRLGAETLPRAVTNLEWRSLSNDRRLTONYEAYSHLLCYLRGL 120
QY 121 NROAATAEIRRSIAHFCSTLSQGLGSIAGVMATLGYPLPQPLPTEPPAPAPGPAHSDFIQ 180
DB 121 NROAATAEIRRSIAHFCSTLSQGLGSIAGVMATLGYPLPQPLPTEPPAPAPGPAHSDFIQ 180
QY 181 KMDDFWLKELQTMWRSKADFNRLKKKQPPAAVTLHLGAHGF 225
DB 181 KMDDFWLKELQTMWRSKADFNRLKKKQPPAAVTLHLGAHGF 225

RESULT 7
AAW94466 standard; Protein; 225 AA.
ID AAW94466;
AC AAW94466;
XX 22-APR-1999 (first entry)
DT
DE Human cardiotrophin-like cytokine protein.
XX
XX Human; cardiotrophin-like cytokine; interleukin 6 cytokine family;
XX KM CLC; IL-6; diagnosis; detection; immune system-related disorder;
XX KM cancer; cardiac disorder; heart failure; hypertension; cancer;
XX KM autoimmune disorder; infection.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT 1..27 /label= signal
FT Peptide /label= signal
FT Protein 28..225 /label= Cardiotrophin-like_cytokine
FT Domain 74..79 /label= CD-1
FT /label= "conserved domain"
FT Domain 150..156 /note= "conserved domain"
FT /label= CD-II
FT /note= "conserved domain"
FT Domain 194..198 /label= CD-III
FT /label= "conserved domain"
FT /note= "conserved domain"
XX
XX MO9900415-A1.
XX
XX 07-JAN-1999.
XX
XX 29-JUN-1998; 98WO-US13129.
XX
XX 30-JUN-1997; 97US-0051311.
XX

XX (HUMA-) HUMAN GENOME SCI INC.
XX PA Ruben SM, Shi Y;
XX PI WPI, 1999-095678/08.
XX DR N-PSDB; AAX16161.
XX
XX PT New isolated cardiotrophin-like cytokine nucleic acid - used to
XX PT develop products for treating cardiac and immune system disorders,
XX PT e.g. heart failure, hypertension, cancers, autoimmune disorders and
XX PT infections
XX
XX Claim 1; Fig 1; 103pp; English.
XX
XX CC The present invention relates to a novel cardiotrophin-like cytokine
XX CC (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine
XX CC family. The present sequence represents the human CLC protein. The
XX CC present invention also describes screening methods for identifying
XX CC agonists and antagonists of CLC activity, as well as methods for
XX CC detecting cardiac and immune system-related disorders and
XX CC therapeutic methods for treating cardiac and immune system-related
XX CC disorders, e.g. heart failure, hypertension, cancers, autoimmune
XX CC disorders and infections.
SQ Sequence 225 AA:

Query Match 97.5%; Score 1193; DB 20; Length 225;
Best Local Similarity 96.9%; Pred. No. 5.3e-118;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACLTCTVLMHLPAPALNRTGDPGPGPSIQKTYDITRYLEHQLSLAGT 60
DB 1 MDLRAGDSWGMACLTCTVLMHLPAPALNRTGDPGPGPSIQKTYDITRYLEHQLSLAGT 60
QY 61 YNLYGPPNEPDPNPRLGAETLPRAVTNLEWRSLSNDRRLTONYEAYSHLLCYLRGL 120
DB 61 YNLYGPPNEPDPNPRLGAETLPRAVTNLEWRSLSNDRRLTONYEAYSHLLCYLRGL 120
QY 121 NROAATAEIRRSIAHFCSTLSQGLGSIAGVMATLGYPLPQPLPTEPPAPAPGPAHSDFIQ 180
DB 121 NROAATAEIRRSIAHFCSTLSQGLGSIAGVMATLGYPLPQPLPTEPPAPAPGPAHSDFIQ 180
QY 181 KMDDFWLKELQTMWRSKADFNRLKKKQPPAAVTLHLGAHGF 225
DB 181 KMDDFWLKELQTMWRSKADFNRLKKKQPPAAVTLHLGAHGF 225

RESULT 8
AA87813 standard; Protein; 225 AA.
ID AA87813
XX
XX AA87813;
AC
XX
XX 24-AUG-2000 (first entry)
DT
DE Human NNT-1 protein.
XX
XX NNT-1; human; neurotrophic factor; neurotrophic; neuroprotective; treatment;
XX KM anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
XX KM nervous system degeneration; Alzheimer's disease; Parkinson's disease;
XX KM amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
XX KM Huntington's disease; peripheral neuropathy; neural retina degeneration;
XX KM retinopathy; immune disorder; hematopoietic disorder.
XX
XX Homo sapiens.
OS
XX
XX US6054294-A.
XX
XX 25-APR-2000.
XX
XX 12-DEC-1997; 97US-0988819.
XX

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Db      1 MDLRAGDSWGMGLACCTVLMHLPVAPALNRTGDPGPGSIQKTYDLYRLEHQRLSLAGT 60
Qy      61 YLNTLGPPFPNPDNPPLGAEITLPRAVNLKLVWRSINDRLRLTONYEAYSHLLCYLRGL 120
Db      61 YLNTLGPPFPNPDNPPLGAEITLPRAVNLKLVWRSINDRLRLTONYEAYSHLLCYLRGL 120
Qy      121 NROAATLRLSLAHFCTSLQGLSAGVWATLGYPLPOPLPGTEPAMAPGPAHSDFLQ 180
Db      121 NROAATLRLSLAHFCTSLQGLSAGVWATLGYPLPOPLPGTEPAMAPGPAHSDFLQ 180
Qy      181 KMDDFWLKELQTVLMRSKADFNRLKKKQPPAASVTTLHLBAHG 225
Db      181 KMDDFWLKELQTVLMRSKADFNRLKKKQPPAASVTTLHLBAHG 225

RESULT 5
AAM29715
ID      AAM29715 standard; Protein; 225 AA.
AC      AAM29715;
DT      09-NOV-1998 (first entry)
DE      Human neurotrophic factor NNT-1.
XX      NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
KW      Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW      amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW      peripheral neuropathy; dystrophy; neural retina degeneration;
KW      common variable immunodeficiency; CVID; selective IGA deficiency;
KW      hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
KW      therapy.
OS      Homo sapiens.
XX      Key      Location/Qualifiers
FH      Peptide      1..27
FT      /label= Sig_peptide
FT      Protein      28..225
FT      /label= Mac_protein
XX      WO9833922-A1.
XX      06-AUG-1998.
XX      02-FEB-1998; 98WO-US02363.
XX      30-JAN-1998; 98US-0016534.
XX      03-FEB-1997; 97US-0792019.
XX      (AMGE-) AMGEN INC.
XX      Chang M, Elliot GS, Sarmiento U, Senaldi G;
XX      WPI: 1998-437475/37.
XX      N-PSDB; AAV47510, AAV47511.
XX      Newly isolated nucleic acid encoding human or murine neurotrophic
XX      factor NNT-1 - useful for treatment of neurological and
XX      immunological diseases or inflammation, also as vaccine adjuvant
XX      Claim 12; Fig 3; 120pp; English.
XX      This is the amino acid sequence of a novel neurotrophic factor,
XX      designated NNT-1, that is a growth factor for neurons and for B or
XX      T cells. It was deduced from isolated cDNA (see AAV47510) and
XX      genomic DNA (see AAV47511) clones. Vectors containing the cDNA or
XX      genomic DNA and host cells are provided for use in the production
XX      of NNT-1 polypeptides. These are used to treat: (1) neurological
XX      or immunological diseases, specifically Alzheimer's, Parkinson's
XX      or Huntington's diseases, amyotrophic lateral sclerosis,
XX      Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and

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CC      degeneration of the neural retina, or conditions characterised by T
CC      or B cell defects, e.g. common variable immunodeficiency (CVID),
CC      selective Iga deficiency, hypogammaglobulinaemia and X-linked
CC      agammaglobulinaemia (claimed), but many others disclosed; and (ii)
CC      inflammation. NNT-1 is also able to boost immunoreactivity and
CC      antibody production following vaccination, and, since it inhibits
CC      tumour necrosis factor production, it may also be useful for
CC      treating sepsis. In addition, cells that have been engineered to
CC      express NNT-1 can be implanted, or nucleic acids are delivered in
CC      gene therapy vectors.
XX      SQ      Sequence      225 AA;
XX      Query Match      97.5%; Score 1193; DB 19; Length 225;
XX      Best Local Similarity 96.9%; Pred. No. 5.3e-118;
XX      Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy      1 MDLRAGDSWGMGLACCTVLMHLPVAPALNRTGDPGPGSIQKTYDLYRLEHQRLSLAGT 60
Db      1 MDLRAGDSWGMGLACCTVLMHLPVAPALNRTGDPGPGSIQKTYDLYRLEHQRLSLAGT 60
Qy      61 YLNTLGPPFPNPDNPPLGAEITLPRAVNLKLVWRSINDRLRLTONYEAYSHLLCYLRGL 120
Db      61 YLNTLGPPFPNPDNPPLGAEITLPRAVNLKLVWRSINDRLRLTONYEAYSHLLCYLRGL 120
Qy      121 NROAATLRLSLAHFCTSLQGLSAGVWATLGYPLPOPLPGTEPAMAPGPAHSDFLQ 180
Db      121 NROAATLRLSLAHFCTSLQGLSAGVWATLGYPLPOPLPGTEPAMAPGPAHSDFLQ 180
Qy      181 KMDDFWLKELQTVLMRSKADFNRLKKKQPPAASVTTLHLBAHG 225
Db      181 KMDDFWLKELQTVLMRSKADFNRLKKKQPPAASVTTLHLBAHG 225

RESULT 6
AAM56141
ID      AAM56141 standard; Protein; 225 AA.
AC      AAM56141;
DT      13-JUL-1998 (first entry)
DE      Amino acid sequence of human neurotrophic factor NNT-1.
XX      Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
KW      treatment; neurological disease; degeneration; Parkinson's disease;
KW      amyotrophic lateral sclerosis; ALS; Alzheimers's disease; stroke.
XX      Homo sapiens.
XX      OS      Homo sapiens.
XX      Key      Location/Qualifiers
FH      Peptide      1..27
FT      /note= "signal peptide"
FT      Protein      28..225
FT      /note= "mature protein"
XX      US5741772-A.
XX      21-APR-1998.
XX      03-FEB-1997; 97US-0792019.
XX      03-FEB-1997; 97US-0792019.
XX      (AMGE-) AMGEN INC.
XX      Chang M;
XX      WPI: 1998-260526/23.
XX      N-PSDB; AAV22652.
XX      Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
XX      useful for stimulating growth of motor and sympathetic neurons

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KW Huntington's disease; peripheral neuropathy; neural retina degeneration;
XX retinopathy; immune disorder; hematopoietic disorder.
XX
OS Mus sp.
XX
PN US6054294-A.
XX
PD 25-APR-2000.
XX
PF 12-DEC-1997; 97US-0988819.
XX
PR 03-FEB-1997; 97US-0792019.
XX
PA (AMGE-) AMGEN INC.
XX
PI Chang M;
XX
DR WPI; 2000-338492/29.
XX
DR N-PSDB; AAA39483.
XX
PT New nucleic acids encoding neurotrophic factors useful for stimulating
PT growth of motor or sympathetic neurons for treating neuron cell damage
PT
XX
PS Claim 2b; Fig 5; 42pp; English.
XX
CC This invention describes a novel nucleic acid molecule (I) encoding a
CC novel neurotrophic factor (NNT-1) (II) which has neurotrophic,
CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
CC ophthalmological activity. (I) is useful for producing NNT-1
CC polypeptides which are useful for treating patients in whom various
CC cells of the central, autonomic, or peripheral nervous system have
CC degenerated and/or have been damaged by congenital disease, trauma,
CC mechanical damage, surgery, stroke, ischemia, infection, metabolic
CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
CC proteins are used to treat diseases like Alzheimer's, Parkinson's,
CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
CC disease, peripheral neuropathy induced by diabetes or other metabolic
CC disorders, and/or dystrophies or degeneration of the neural retina such
CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
CC night blindness, progressive cone-rod degeneration, immune disorders and
CC hematopoietic disorders. (II) is effective in treating neurological
CC conditions and promotes neuron regeneration. Neural functions are
CC effectively restored in patients suffering from various neurological
CC disorders. This sequence represents the murine NNT-1 protein described in
CC the method of the invention.
XX
XX
SQ Sequence 225 AA;
XX
Query Match 100.0%; Score 1224; DB 21; Length 225;
Best Local Similarity 100.0%; Pred. No. 2,7e-121;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQSLAGT 60
DB 1 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQSLAGT 60
QY 61 YANVIGPPNEPDPNPRGAEPLPRATNLEWMSLNDRLKLTQNYEAYSHLCTLRGL 120
DB 61 YANVIGPPNEPDPNPRGAEPLPRATNLEWMSLNDRLKLTQNYEAYSHLCTLRGL 120
QY 121 NROQATAELERRSLAHCCTSLQGLGSIAGVMATLGVLPOLPGREPPAAPPAHSDFIQ 180
DB 121 NROQATAELERRSLAHCCTSLQGLGSIAGVMATLGVLPOLPGREPPAAPPAHSDFIQ 180
QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLEAHGF 225
DB 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLEAHGF 225
RESULT 4
AAU78177
ID AAU78177 standard; Protein; 225 AA.

XX
AC AAU78177;
XX
DT 05-JUN-2002 (first entry)
XX
DE Mouse novel neurotrophic factor NNT1.
XX
KW Mouse; NNT1; neurotrophic factor; IGF-related disease;
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW vascular stenosis; rheumatoid arthritis; psoriatic arthritis;
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.
XX
OS Mus sp.
XX
PN WO200215977-A2.
XX
PD 26-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US25906.
XX
PR 18-AUG-2000; 2000US-226436P.
XX
PR 16-AUG-2001; 2001US-0931704.
XX
PA (AMGE-) AMGEN INC.
XX
PI Senaldi G;
XX
DR WPI; 2002-280867/32.
XX
DR N-PSDB; ABK11649.
XX
PT Treating Immunoglobulin E-related disease, modulating IGE levels in a
PT patient, preventing IGE-related disease and treating allergic diseases,
PT involves administering NNT-1 inhibitor to a patient
XX
PS Claim 2; Fig 5; 63pp; English.
XX
CC The invention relates to treating Immunoglobulin E (IGE)-related disease,
CC modulating IGE levels in a patient, preventing an IGE-related disease,
CC and treating allergic diseases, comprising administering a
CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
CC inhibitor to a patient. Also included are a method of diagnosing an
CC IGE-related disease or susceptibility to an IGE-related disease, by
CC determining the presence or amount of expression of an NNT1 polypeptide
CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
CC occurring variant, and diagnosing an IGE-related disease or
CC susceptibility of an IGE-related disease based on the presence or amount
CC of expression of the polypeptide and a pharmaceutical composition for use
CC in treating IGE-related disease, comprising the NNT1 inhibitor.
CC The NNT1 inhibitor is useful for preventing and treating IGE-related
CC disease, modulating IGE levels, and treating allergic diseases e.g.
CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,
CC pollinosis, asthma, immune diseases and disorders, diseases involving
CC abnormal cell proliferation including cancer, arteriosclerosis and
CC vascular stenosis, diseases and conditions relating to dysfunction of
CC immune system including rheumatoid arthritis, psoriatic arthritis,
CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,
CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
CC bowel disease, transplant rejection, and graft versus host disease, and
CC reproductive diseases and disorders including infertility, miscarriage,
CC preterm labour and delivery, and endometriosis. The present sequence
CC represents Mouse NNT1.
XX
XX
SQ Sequence 225 AA;
XX
Query Match 100.0%; Score 1224; DB 23; Length 225;
Best Local Similarity 100.0%; Pred. No. 2,7e-121;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQSLAGT 60

PR 30-JAN-1998; 98US-0016534.
 PR 03-FEB-1997; 97US-0792019.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Chang M, Elliot GS, Sarmiento U, Senaldi G;
 PI WPI; 1998-437475/37.
 DR N-PSDB; AAV47512.
 XX

PT Newly isolated nucleic acid encoding human or murine neurotrophic
 PT factor NNT-1 - useful for treatment of neurological and
 PT immunological diseases or inflammation, also as vaccine adjuvant
 XX
 XX Claim 13; Fig 5; 120pp; English.

XX This is the amino acid sequence of a murine neurotrophic factor,
 CC designated NNT-1, that is a growth factor for neurons and for B or
 CC T cells. It was deduced from isolated NNT-1 cDNA (see AAV47512).
 CC Human NNT-1 (see AAV29715) is also provided. Vectors and host cells
 CC for use in the production of human murine recombinant NNT-1.
 CC polypeptides. These are used to treat: (i) neurological or
 CC immunological diseases, specifically Alzheimer's, Parkinson's
 CC or Huntington's diseases, amyotrophic lateral sclerosis,
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
 CC degeneration of the neural retina, or conditions characterized by T
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),
 CC selective IgA deficiency, hypogammaglobulinemia and X-linked
 CC agammaglobulinemia (claimed), but many others disclosed; and (ii)
 CC inflammation. NNT-1 is also able to boost immunoreactivity and
 CC antibody production following vaccination, and, since it inhibits
 CC tumour necrosis factor production, it may also be useful for
 CC treating sepsis. In addition, cells that have been engineered to
 CC express NNT-1 can be implanted, or nucleic acids are delivered in
 CC gene therapy vectors.
 XX

SQ Sequence 225 AA;

Query Match 100.0%; Score 1224; DB 19; Length 225;
 Best Local Similarity 100.0%; Pred. No. 2.7e-121;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MDLRAGDSWGMALACTCTVLMHLPAYPALNRTGDPGPGPSIOKTYDLTRYLSEHQLSLAGT 60
 QY 61 YLNYLGPPNPEDFNPRLGAEITLPRAVNLVWRSLSNDRRLRLQNYEAYSHLLCYLRGL 120
 DB 61 YLNYLGPPNPEDFNPRLGAEITLPRAVNLVWRSLSNDRRLRLQNYEAYSHLLCYLRGL 120
 QY 121 NROAATAEIRSLAHFCTSLQGLGSLIGVWATTGYPPLPGTEPMAAPGPAHSDFLQ 180
 DB 121 NROAATAEIRSLAHFCTSLQGLGSLIGVWATTGYPPLPGTEPMAAPGPAHSDFLQ 180
 QY 181 KMDDFWLKELQITWLMRSKADFNRLKKKQPPAASVTLLHLEAHGF 225
 DB 181 KMDDFWLKELQITWLMRSKADFNRLKKKQPPAASVTLLHLEAHGF 225

RESULT 2
 AAV56142
 ID AAV56142 standard; Protein: 225 AA.
 XX
 XX AAV56142;
 AC
 XX
 XX 13-JUL-1998 (first entry)
 DT
 XX
 XX

DE Amino acid sequence of murine neurotrophic factor NNT-1.

XX Mouse, neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
 KM treatment; neurological disease; degeneration; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.
 XX

OS Mus sp.

XX Key Location/Qualifiers
 XX 1..27
 FT Peptide /note= "signal peptide"
 FT Protein 28..225
 FT /note= "mature peptide"
 XX

PN US741772-A.

XX 21-APR-1998.

XX 03-FEB-1997; 97US-0792019.

XX 03-FEB-1997; 97US-0792019.

XX (AMGE-) AMGEN INC.

XX Chang M;

DR WPI; 1998-260526/23.
 DR N-PSDB; AAV22654.

PT Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
 PT useful for stimulating growth of motor and sympathetic neurons
 XX
 XX Claim 2; Fig 5; 41pp; English.

XX The present sequence represents a murine neurotrophic factor, designated
 CC NNT-1, which is capable of stimulating growth of motor or sympathetic
 CC neurons. The NNT-1 protein is useful in the treatment of neurological
 CC diseases characterized by the degeneration and death of particular
 CC classes of neurons. These diseases specifically include Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC stroke and various degenerative disorders affecting vision.
 XX

SQ Sequence 225 AA;

Query Match 100.0%; Score 1224; DB 19; Length 225;
 Best Local Similarity 100.0%; Pred. No. 2.7e-121;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MDLRAGDSWGMALACTCTVLMHLPAYPALNRTGDPGPGPSIOKTYDLTRYLSEHQLSLAGT 60
 QY 61 YLNYLGPPNPEDFNPRLGAEITLPRAVNLVWRSLSNDRRLRLQNYEAYSHLLCYLRGL 120
 DB 61 YLNYLGPPNPEDFNPRLGAEITLPRAVNLVWRSLSNDRRLRLQNYEAYSHLLCYLRGL 120
 QY 121 NROAATAEIRSLAHFCTSLQGLGSLIGVWATTGYPPLPGTEPMAAPGPAHSDFLQ 180
 DB 121 NROAATAEIRSLAHFCTSLQGLGSLIGVWATTGYPPLPGTEPMAAPGPAHSDFLQ 180
 QY 181 KMDDFWLKELQITWLMRSKADFNRLKKKQPPAASVTLLHLEAHGF 225
 DB 181 KMDDFWLKELQITWLMRSKADFNRLKKKQPPAASVTLLHLEAHGF 225

RESULT 3
 AAV87814
 ID AAV87814 standard; Protein: 225 AA.
 XX
 XX AAV87814;
 AC
 XX
 XX 24-AUG-2000 (first entry)
 DT
 XX
 XX

DE Murine NNT-1 protein.

XX NNT-1; neurotrophic factor; neurotrophic; neuroprotective; treatment;
 KM anticonvulsant; antiparkinsonian; antidementia; ophthalmological;
 KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine;
 XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2004, 06:14:57 ; Search time 35.5 Seconds
(without alignments)
1006.013 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues 1107863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1224	100.0	225	19	AAW29716
2	1224	100.0	225	19	AAW56142
3	1224	100.0	225	21	AAV7814
4	1224	100.0	225	23	AAV78177
5	1193	97.5	225	19	AAW29715
6	1193	97.5	225	19	AAW56141
7	1193	97.5	225	20	AAW94466
8	1193	97.5	225	21	AAV87813
9	1193	97.5	225	22	AAW63543

10	1193	97.5	225	23	AAU78176	Human novel neurotrophin
11	1193	97.5	225	22	AAW25831	Human protein sequ
12	1181	96.5	223	22	AAE00828	Human cardiocroph
13	1171	95.7	321	22	ABH1896	Human cardiocroph
14	1171	95.7	321	22	AAW79399	Human protein sequ
15	1167	95.3	215	21	AAH1587	Mouse interleukin
16	1164	95.1	260	22	AAW78415	Human protein sequ
17	1136	92.8	215	21	AAH1586	Human interleukin
18	852	69.6	164	22	ABG55577	Human liver peptid
19	852	69.6	164	22	ABH40317	Peptide #7823 enco
20	852	69.6	164	22	ABB24716	Protein #6715 enco
21	852	69.6	164	22	AAW61118	Human brain expres
22	852	69.6	164	22	AAW73827	Human bone marrow
23	852	69.6	164	22	AAW20115	Peptide #6549 enco
24	852	69.6	164	22	AAW34012	Peptide #8049 enco
25	852	69.6	164	23	ABG43716	Human peptid enco
26	156.5	12.8	208	20	AAV09197	Human DNAX interle
27	154	12.6	208	20	AAV09196	Human DNAX interle
28	110.5	9.0	203	16	AAH83965	Mouse cardiac hype
29	110.5	9.0	203	17	AAH88204	Human cardiocroph
30	110.5	9.0	203	18	AAW29237	Human cardiocroph
31	92.5	7.6	243	22	AAU09153	Human cytokine zal
32	92.5	7.6	243	22	AAH20277	Human interleukin
33	92.5	7.6	243	23	ABG32291	Human IL-D80 prote
34	92.5	7.6	243	23	AAU76375	Human helical prot
35	92.5	7.6	243	24	ABG75877	Human cytokine IL-
36	92	7.5	332	21	AAW40321	Arabidopsis thalia
37	92	7.5	332	21	AAW40321	Arabidopsis thalia
38	91.5	7.5	201	16	AAH83967	Human cardiac hype
39	91.5	7.5	201	18	AAW29238	Human cardiocroph
40	91.5	7.5	201	20	AAV06490	Human tumour-assoc
41	91.5	7.5	201	21	AAH27662	Human protein PRO8
42	91.5	7.5	201	21	AAH13004	Human cardiocroph
43	91.5	7.5	201	21	AAV93697	Human cardiocroph
44	91.5	7.5	201	21	AAH7818	Amino acid sequenc
45	91.5	7.5	201	22	AAW50994	Human cardiocroph

ALIGNMENTS

AAW29716	standard; Protein; 225 AA.
AAW29716	
AAW29716	
09-NOV-1998	(first entry)
Mouse neurotrophic factor NNT-1.	
NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; peripheral neuropathy; dystrophy; neural retina degeneration; common variable immunodeficiency; CVID; selective IGA deficiency; hypogammaglobulinaemia; X-linked agammaglobulinaemia; antisepic; therapy.	
Mus sp.	
Key	Location/Qualifiers
Peptide	1..27
Protein	/label= Sig_peptide
	28..225
	/label= Mat_protein
W09833922-A1.	
06-AUG-1998.	
02-FEB-1998;	98WO-US02363.

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DB 162 LPEEBEEEEEBERKGLPGALGSAQVPAQVWPQLSTYRLHLSLEVLSSAVREL 221
QY 203 NRLKK 207
DB 222 LLLSK 226

RESULT 12
US-10-000-776-6
; Sequence 6, Application US/10000776
; Publication No. US20020164609A1
; GENERAL INFORMATION:
; APPLICANT: Timanz, Jacqueline C.
; APPLICANT: Pelanz, Stefan K.-H.
; APPLICANT: Kaetelein, Robert A.
; APPLICANT: Bazan, Jose F.
; APPLICANT: Kennick, Donna
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Cheung, Jeanne
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX01040K3
; CURRENT APPLICATION NUMBER: US/10/000,776
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/791,497
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-776-6

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Best Local Similarity 23.3%; Pred. No. 0.6;
Matches 57; Conservative 26; Mismatches 105; Indels 57; Gaps 9;
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DB 1 MCGTGGDLCWRSLTLPLLVQAGVWGPRPPG-----RPQLSLOLRREFTVSLHL 53
QY 47 TYLLEHQLSLAGTYLN-----YLGPFPNEPDENPRLGAETLPRATVNLGVRSILN 98
DB 54 AKKLSEVVGQAHRAESHLPGVNYLLP-----LG-EQLPVSLSLFOQWRRLS 101
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DB 102 DPERLCFISTLQPFHAPLGGLGTQGRMTNMRMQLMAMRLRLDQLRFLRQVLAAGFN 161
QY 158 LQOP-----LPGTEPMAGPRAHSDPLQCMDFWLLKEQLTLMASAKDF 202
DB 162 LPEEBEEEEEBERKGLPGALGSAQVPAQVWPQLSTYRLHLSLEVLSSAVREL 221
QY 203 NRLKK 207
DB 222 LLLSK 226

RESULT 13
US-10-156-761-11445
; Sequence 11445, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11445
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11445

Query Match 7.6%; Score 92.5; DB 15; Length 860;
Best Local Similarity 27.2%; Pred. No. 3.1;
Matches 56; Conservative 22; Mismatches 101; Indels 27; Gaps 9;
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DB 401 KERTLSALGPGUDSSAEEVRRRVALLADLPBGASAPASVTLARKW--ERPLGRTPS 458
QY 169 WAP--GPAHSDPLQCMDFWLLKEIQ 192
DB 459 PSPSSAPSSDDLRLRLAEWTLSEAE 484

RESULT 14
US-09-901-540-3
; Sequence 3, Application US/09901540
; Patent No. US20020102622A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Goddard, Audrey
; APPLICANT: Lawrence, David A.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret A.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Cardiotrophin-1 Compositions and Methods for the
; FILE REFERENCE: P2533D2
; CURRENT APPLICATION NUMBER: US/09/901,540
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/648,258
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 09/033,114
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: US 08/733,850
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: US 08/443,129
; PRIOR FILING DATE: 1995-05-17
; PRIOR APPLICATION NUMBER: US 08/286,304
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: US 08/233,609
; PRIOR FILING DATE: 1994-04-25
; PRIOR APPLICATION NUMBER: US 60/113,296
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 3
; LENGTH: 201

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APPLICANT: Zehnusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIORITY APPLICATION NUMBER: 60/251,660
PRIORITY FILING DATE: 2000-12-06
PRIORITY APPLICATION NUMBER: 60/255,029
PRIORITY FILING DATE: 2000-12-12
PRIORITY APPLICATION NUMBER: 60/260,326
PRIORITY FILING DATE: 2001-01-08
PRIORITY APPLICATION NUMBER: 60/263,800
PRIORITY FILING DATE: 2001-01-24
PRIORITY APPLICATION NUMBER: 60/269,942
PRIORITY FILING DATE: 2001-02-20
PRIORITY APPLICATION NUMBER: 60/286,183
PRIORITY FILING DATE: 2001-04-24
PRIORITY APPLICATION NUMBER: 60/313,627
PRIORITY FILING DATE: 2001-08-20
PRIORITY APPLICATION NUMBER: 60/318,712
PRIORITY FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
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TYPE: PRT
ORGANISM: Mus musculus
US-10-231-913-98
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Sequence 5; Application US/09810052
Patent No. US2002009755A1
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: HELICAL PROTEIN ZALPHA51
FILE REFERENCE: 00-24
CURRENT APPLICATION NUMBER: US/09/810,052
CURRENT FILING DATE: 2001-03-16
PRIORITY APPLICATION NUMBER: 60/190,410
PRIORITY FILING DATE: 2000-03-17
PRIORITY APPLICATION NUMBER: 60/199,443
PRIORITY FILING DATE: 2000-04-25
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US-09-810-052-5
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DB 162 LPEEEEEEERKSKGLLPALGSLQGPVQVSWPQLSTYRLHSLIELVLSRAVRL 221
QY 203 NRIKK 207
DB 222 LLSKK 226
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RESULT 11
US-09-791-497-8
Sequence 8; Application US/09791497
Publication No. US20030008343A1
GENERAL INFORMATION:
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APPLICANT: Timans, Jacqueline C.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
APPLICANT: Peltanz, Stefan
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
FILE REFERENCE: DX01040K2
CURRENT APPLICATION NUMBER: US/09/791,497
CURRENT FILING DATE: 2001-02-22
PRIORITY APPLICATION NUMBER: 09/627,897
PRIORITY FILING DATE: 2000-07-27
PRIORITY APPLICATION NUMBER: 60/146,581
PRIORITY FILING DATE: 1999-07-30
PRIORITY APPLICATION NUMBER: 60/147,763
PRIORITY FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 243
TYPE: PRT
ORGANISM: primate; surmised Homo sapiens
US-09-791-497-8
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Best Local Similarity 23.3%; Pred. No. 0.6;
Matches 57; Conservative 26; Mismatches 105; Indels 57; Gaps 9;
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QY 1 MDLRAGD-SWGMILACTVTL-----WHLPAVALNRRTGDPGPGSIQK-----TYDL 46
DB 1 MCGTADDLGKRLSLLPLLVQAGVGFPRPG-----RPQSLQELRREFVTSIHL 53
QY 47 TRYLEHQLSLAGTYLN-----YLGPFPNEPDPNPRLGAEITLPRATVNLVWMSLN 98
DB 54 ARKLSEVRGQAHRAESHLPGVNLYLP-----LG-EQLPDVSLTFQAWRRLS 101
QY 99 DRLRLTONYEAVSHLLCYLRGLNRQAATAELESLAHFCTSLQGLSIGVMAATLGYP 157
DB 102 DPERLCFISTTLQPFHAPLGLGTQGRWTNMRMQLMAMRLDLRLQRRHLRFQVLAAGFN 161
QY 158 LPOP-----LPGTEPAMAPASDPLQKMDFFWLKELQWLMRSAXDF 202
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 40014
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005849.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
OTHER INFORMATION: EST HUMAN HIT: A1752561.1, EVALUE 3.00e-66
OTHER INFORMATION: SWISSPROT HIT: Q63086, EVALUE 8.00e-03
US-09-864-761-40014

Query Match 69.6%; Score 852; DB 9; Length 164;
Best Local Similarity 95.1%; Pred. No. 1.1e-76;
Matches 156; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 62 LNTLGPPEPDNPRLGAEPLPRAVNLVWRSINDRLTONTYAVSHLLCYLRGIN 121
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DB 61 RQATTELRSLAHFCTSLQGLLGSAGWATGYPPLPPTTEPAMAGPASHDFLOK 120
QY 182 MDDFWLKELOTLWMSAKDFNRLKKKMOPPASVTLHEAHGF 225
DB 121 MDDFWLKELOTLWMSAKDFNRLKKKMOPPASVTLHEAHGF 164

RESULT 5
US-10-212-793-3
Sequence 3: Application US/10212793
Publication No. US20030087395A1
GENERAL INFORMATION:
APPLICANT: Shi et al.
FILE REFERENCE: PF385D1C1
CURRENT APPLICATION NUMBER: US/10/212,793
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 09/438,299
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/106,182
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: US 60/051,311
PRIOR FILING DATE: 1997-06-30
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 3
LENGTH: 203
TYPE: PRT
ORGANISM: rattus norvegicus
US-10-212-793-3

Query Match 9.7%; Score 118.5; DB 15; Length 203;
Best Local Similarity 27.5%; Pred. No. 0.0012;
Matches 49; Conservative 26; Mismatches 84; Indels 19; Gaps 6;
QY 40 IOKTYDLTRYLEHQRLSLAGTYLNTLGPPEPDNPRL--GAETLPRAVNLVWRS 96
DB 27 IROTNLRLRLTKYADQLLEEVYQOGSEFGFPGFSPRLPLAGLSGAPASHAGLPV-- 83
QY 97 LNDRLTONTYAVSHLLCYLRGINRQA-----TAEIRSLAHFCTSLQGLLGSAGW 151
DB 84 -SERLR--ODAAALSLPALDAVRRQAEINPRAPRLRSLIEDARQVRAAGAAVETVL 140
QY 152 ATLGY-----PLPPLPTEPAMAGPASHDFLOKMDFWLKELOTLWMSAKDFNRL 205

DB 141 AALGAARGPVEPVP-ATSALEFTSNSAGVFSKVLGHVCGIYGEWVRTEGDLQCL 197

RESULT 6
US-09-896-856-3
Sequence 3: Application US/09896856
Patent No. US20020137189A1
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
Chien, Kenneth
King, Kathleen
Pennica, Diane
Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/896,856
FILING DATE: 29-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/733,850
FILING DATE: 18-OCT-1996
APPLICATION NUMBER: US 08/471,112
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: 08/233,609
FILING DATE: 25-APR-1994
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: 08/443129
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P0894PID2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2066
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: Amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-896-856-3

Query Match 9.0%; Score 110.5; DB 10; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.0077;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;
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QY 97 LNDRLTONTYAVSHLLCYLRGINRQA-----TAEIRSLAHFCTSLQGLLGSAGW 151
DB 84 -SERLR--ODAAALSLPALDAVRRQAEINPRAPRLRSLIEDARQVRAAGAAVETVL 140
QY 152 ATLGYPLPPLPTEPAMAGPASHDFLOKMDFWLKELOTLWMSAKDFNRL 205

Db 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAASVTTLHAHGF 225

RESULT 2
US-09-931-704-2
Sequence 2, Application US/09931704
Patent No. US20020041873A1
GENERAL INFORMATION:
APPLICANT: Senaldi, Giorgio
TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using N
FILE REFERENCE: A-695
CURRENT APPLICATION NUMBER: US/09/931,704
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/226,436
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent in version 3.1
SEQ ID NO 2
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
US-09-931-704-2

Query Match Best Local Similarity 97.5%; Score 1193; DB 9; Length 225;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRGDPGPGPSIQKTYDLTRYLEHQRLSLAGT 60
Db 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRGDPGPGPSIQKTYDLTRYLEHQRLSLAGT 60

Qy 61 YLNYIGPPENEDFPNPRPGAETLPRAVTNLEWMSLNDRLRLTONYEAYSHLLCYLRL 120
Db 61 YLNYIGPPENEDFPNPRPGAETLPRAVTNLEWMSLNDRLRLTONYEAYSHLLCYLRL 120

Qy 121 NROAATALRSLAHFCTSLGGLGSLAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 180
Db 121 NROAATALRSLAHFCTSLGGLGSLAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 180

Qy 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAASVTTLHAHGF 225
Db 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAASVTTLHAHGF 225

RESULT 3
US-10-212-793-2
Sequence 2, Application US/10212793
Patent No. US20030087395A1
GENERAL INFORMATION:
APPLICANT: Shi et al.
TITLE OF INVENTION: Cardiotrophin-Like Cytokine
FILE REFERENCE: PF385DICI
CURRENT APPLICATION NUMBER: US/10/212,793
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 09/438,299
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/106,182
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: US 60/051,311
PRIOR FILING DATE: 1997-06-30
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 2
LENGTH: 225
TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: signal
LOCATION: (-27)..(-1)
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(198)

US-10-212-793-2

Query Match Best Local Similarity 97.5%; Score 1193; DB 15; Length 225;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRGDPGPGPSIQKTYDLTRYLEHQRLSLAGT 60

Qy 61 YLNYIGPPENEDFPNPRPGAETLPRAVTNLEWMSLNDRLRLTONYEAYSHLLCYLRL 120
Db 61 YLNYIGPPENEDFPNPRPGAETLPRAVTNLEWMSLNDRLRLTONYEAYSHLLCYLRL 120

Qy 121 NROAATALRSLAHFCTSLGGLGSLAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 180
Db 121 NROAATALRSLAHFCTSLGGLGSLAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 180

Qy 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAASVTTLHAHGF 225
Db 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAASVTTLHAHGF 225

RESULT 4
US-09-864-761-40014
Sequence 40014, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00671
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2001-01-29

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2004, 06:17:01 ; Search time 33 Seconds
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1427.606 Million cell updates/sec

Title: US-09-931-704-5
Perfect score: 1224
Sequence: 1 MBLRAGDSWGMCLCTVLM.....KKKMPAASVTLHLEAHGF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues
Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1193	97.5	225	US-09-931-704-2	Sequence 2, Appl1
3	1193	97.5	225	US-10-212-793-2	Sequence 2, Appl1
4	852	69.6	164	US-09-864-761-40014	Sequence 40014, A
5	118.5	9.7	203	US-10-212-793-3	Sequence 3, Appl1
6	110.5	9.0	203	US-09-896-886-3	Sequence 3, Appl1
7	110.5	9.0	203	US-10-407-303-3	Sequence 3, Appl1
8	110.5	9.0	203	US-10-107-931-3	Sequence 3, Appl1
9	93	7.6	727	US-10-231-913-98	Sequence 98, Appl1
10	92.5	7.6	243	US-09-810-052-5	Sequence 5, Appl1
11	92.5	7.6	243	US-09-791-497-8	Sequence 8, Appl1
12	92.5	7.6	243	US-10-000-776-6	Sequence 6, Appl1
13	92.5	7.6	860	US-10-156-761-11445	Sequence 11445, A
14	91.5	7.5	201	US-09-901-540-3	Sequence 3, Appl1
15	91.5	7.5	201	US-09-896-856-8	Sequence 8, Appl1

16	91.5	7.5	201	US-09-901-257-3	Sequence 3, Appl1
17	91.5	7.5	201	US-10-407-303-8	Sequence 8, Appl1
18	91.5	7.5	201	US-10-107-931-8	Sequence 8, Appl1
19	91.5	7.5	201	US-10-212-793-4	Sequence 4, Appl1
20	90	7.4	195	US-09-770-361-5	Sequence 5, Appl1
21	90	7.4	195	US-10-281-643-5	Sequence 5, Appl1
22	90	7.4	195	US-10-383-916-5	Sequence 5, Appl1
23	90	7.4	195	US-10-226-759-5	Sequence 5, Appl1
24	87	7.1	242	US-09-791-497-2	Sequence 2, Appl1
25	87	7.1	242	US-10-000-776-2	Sequence 2, Appl1
26	86.5	7.1	285	US-10-156-761-9399	Sequence 9399, Ap
27	86.5	7.1	1429	US-10-028-374-3	Sequence 3, Appl1
28	86.5	7.1	1429	US-10-183-770-3	Sequence 3, Appl1
29	86	7.0	232	US-09-810-052-2	Sequence 2, Appl1
30	85.5	7.0	389	US-10-369-493-22941	Sequence 22941, A
31	82	6.7	450	US-10-156-761-7904	Sequence 7904, Ap
32	81.5	6.7	348	US-09-730-617-2	Sequence 2, Appl1
33	81	6.6	842	US-10-156-761-9089	Sequence 9089, Ap
34	80.5	6.6	379	US-09-861-289-16	Sequence 16, Appl
35	80.5	6.6	379	US-09-860-846-16	Sequence 16, Appl
36	80.5	6.6	379	US-09-988-384B-16	Sequence 16, Appl
37	80.5	6.6	379	US-09-836-821-16	Sequence 16, Appl
38	80.5	6.6	379	US-10-271-889-16	Sequence 16, Appl
39	80.5	6.6	3782	US-09-861-289-4	Sequence 4, Appl1
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41	80.5	6.6	3782	US-09-988-384B-4	Sequence 4, Appl1
42	80.5	6.6	3782	US-09-836-821-4	Sequence 4, Appl1
43	80.5	6.6	3782	US-10-271-889-4	Sequence 4, Appl1
44	80	6.5	275	US-10-156-761-12256	Sequence 12256, A
45	80	6.5	876	US-10-074-511-110	Sequence 110, App

ALIGNMENTS

RESULT 1
US-09-931-704-5
; Sequence 5, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Murine
US-09-931-704-5

Query Match	Score	DB 9;	Length	DB 225;
Best Local Similarity	100.0%;	Pred. No. 1.8e-113;		
Matches 225;	Conservative	0;	Mismatches 0;	Gaps 0;
QY	1	MLRAGDSWGMCLCTVLMHLPALNRTSDPGPSPISOKTYDUTRYLHQLSLACT	60	
DB	1	MLRAGDSWGMCLCTVLMHLPALNRTSDPGPSPISOKTYDUTRYLHQLSLACT	60	
QY	61	YLVNIGPPNEBDFNPRIAGATLPRATVNLVWMSLNDRLTLTONVEYSHLLCYRLGL	120	
DB	61	YLVNIGPPNEBDFNPRIAGATLPRATVNLVWMSLNDRLTLTONVEYSHLLCYRLGL	120	
QY	121	NFOAATAEIRSLAHCCTSLGGLSAGVATTCGYLPOLPGTEPAPAPASDFIQ	180	
DB	121	NFOAATAEIRSLAHCCTSLGGLSAGVATTCGYLPOLPGTEPAPAPASDFIQ	180	
QY	181	KMDDEWLKLEQITWLMRSKDFNRLLKKKMPAASVTLHLEAHGF	225	

TELEPHONE: 415/423-8888
TELEFAX: 415/952-9881

TOPOLOGY: linear

TOPOLOGY: linear

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286.304
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 894P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-286-304-3

Query Match 9.0%; Score 110.5; DB 1; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.00067;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY 40 IQKTYDLTRYLEHQLSLAGTYLNYLGPPFNEPDNPRL---GAEUPLRATVNLVWRS 96
DB 27 IROTHNLARLLTKYAEQLLEEVYQGGEPFGLPGSPRLPLAGLSGAPSHAGLPV--- 83
QY 97 LNDRLRLTONYEAHYSHLLCYRGLNRQA-----TAEIRSLAHFCTSLQGLLSIAGVM 151
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DB 141 AALGAANG--PGPEPVVATLFTANSTAGIFSARVGLGHVGLYGEWVSRTEGDLGL 197

RESULT 12
US-08-442-745-3
Sequence 3, Application US/08442745

Patent No. 5624806
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Penicka, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,745
FILING DATE: 17-may-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/233609

FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-442-745-3

Query Match 9.0%; Score 110.5; DB 1; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.00067;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY 40 IQKTYDLTRYLEHQLSLAGTYLNYLGPPFNEPDNPRL---GAEUPLRATVNLVWRS 96
DB 27 IROTHNLARLLTKYAEQLLEEVYQGGEPFGLPGSPRLPLAGLSGAPSHAGLPV--- 83
QY 97 LNDRLRLTONYEAHYSHLLCYRGLNRQA-----TAEIRSLAHFCTSLQGLLSIAGVM 151
DB 84 -SERLR--QDAALSVLPALDAVRRQAELNPRAPRLRLSLIEDAPARQVRAALGAAVETVL 140
QY 152 ATLGVPPLQPLPGTEPA-----WAPGPAHSDFLQKMDPFWLKEIQTWLMSAKDPNRL 205
DB 141 AALGAANG--PGPEPVVATLFTANSTAGIFSARVGLGHVGLYGEWVSRTEGDLGL 197

RESULT 13
US-08-443-129-3
Sequence 3, Application US/08443129

Patent No. 5627073
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Penicka, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,129
FILING DATE: 17-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 304
FILING DATE: (null)

```

; Patent No. 5534615
; GENERAL INFORMATION:
APPLICANT: Baker, Joffe
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,609
FILING DATE: 25-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 894
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-233-609-3

Query Match          9.0%; Score 110.5; DB 1; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.00067;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY  IOKYYDRLRYLEHQRSLAGTYLNTLGPPPEEDFNPRLL--GAEIPLRAVLNEVRS 96
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  27 IRQTNNLRARLLTKYAEOQLLEEVOQGEGPGLPGSPRPRLPLAGLSGPAPSHAGLPV--- 83
   ||::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY  LNDRLRLQNTEAVSYHLICYLKGLNRQA-----TAEIRRSILAHRCTSLOGILGSIAQVM 151
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  84 -SERLR--QDAALASVLPALLDAVARRQAEINPRAPRLIRSRSEDARQVRALGAAVEIVL 140
   :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY  152 ATLGYPFLPQLPGTEPA-----WAPGASHDFLOKMDFFWLKELQTLWMSSAKDPNRL 205
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  141 AALGMAARG--PGPEPVATLTFTANSTRAGIFSAKVLAGFHVCGLGGEWVSRTBEDLQGL 197
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
US-08-444-083-3
Sequence 3, Application US/08444083
Patent No. 5571675
GENERAL INFORMATION:
APPLICANT: Baker, Joffe
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:

```

```

ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M5-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,083
FILING DATE: 17-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894PIDS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-444-083-3

Query Match          9.0%, Score 110.5; DB 1; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.00067;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY  ICKTVYDLTRYLYEHQLRLSLAGTYLNYLGPPPEPDNPRL---GAEFLPRATVNLVEVRS 96
DB  27 IRQHNNLARLLTKYAEDLEEYVOQGEPGLPGSPPLRLLAGISGPASHAGLPV--- 83
QY  97 LNDLRLTONTNENAVSHLLCYRGDGNROA-----TAEIRSLAFCTSLQGLSIGVM 151
DB  84 -SEILR--QDAALASVLPALLDAYRRKQDALNPAPRLRLSELDAQAQVRLLGAAYEIVL 140
QY  152 ATIGYPPLDPQLPSTEPA----WAPGAHSDFLQKMDFWMLKLQTWLMSAKDFNRL 205
DB  141 AALGAARG--FGPEPYVTATLFPANSTAGIFSAKVIGFYHCGLYGEWVSRTBEDLGL 197

RESULT 11
US-08-286-304-3
Sequence 3, Application US/08286304
Patent No. 5571893
GENERAL INFORMATION:
APPLICANT: Baker, Joffe
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

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Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMGLACTVLMHLPAVPALNRITGDPGPGPSIQKTYDLTRYLHQLSLAGT 60
DB 1 MDLRAGDSWGMGLACTVLMHLPAVPALNRITGDPGPGPSIQKTYDLTRYLHQLSLAGT 60

QY 61 YLNYLGPPFPNEBDFPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAYSHLCTYLRGL 120
DB 61 YLNYLGPPFPNEBDFPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAYSHLCTYLRGL 120

QY 121 NRQAATAEIRSLAHFCTSLQGLGSIAGWATIGYLPQPLPGTEPMAAPGPAHSDFLQ 180
DB 121 NRQAATAEIRSLAHFCTSLQGLGSIAGWATIGYLPQPLPGTEPMAAPGPAHSDFLQ 180

QY 181 KMDDFWLLKEIQTWLMRSADFNRLKKKQPPAAAVTLHLGANGF 225
DB 181 KMDDFWLLKEIQTWLMRSADFNRLKKKQPPAAAVTLHLGANGF 225

RESULT 7

US-09-016-534-2
Sequence 2, Application US/09016534

Patent No. 6143874
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: ELLIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-534-2

Query Match 97.5%; Score 1193; DB 3; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.7e-119;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMGLACTVLMHLPAVPALNRITGDPGPGPSIQKTYDLTRYLHQLSLAGT 60
DB 1 MDLRAGDSWGMGLACTVLMHLPAVPALNRITGDPGPGPSIQKTYDLTRYLHQLSLAGT 60

QY 61 YLNYLGPPFPNEBDFPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAYSHLCTYLRGL 120
DB 61 YLNYLGPPFPNEBDFPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAYSHLCTYLRGL 120

QY 121 NRQAATAEIRSLAHFCTSLQGLGSIAGWATIGYLPQPLPGTEPMAAPGPAHSDFLQ 180
DB 121 NRQAATAEIRSLAHFCTSLQGLGSIAGWATIGYLPQPLPGTEPMAAPGPAHSDFLQ 180

QY 181 KMDDFWLLKEIQTWLMRSADFNRLKKKQPPAAAVTLHLGANGF 225
DB 181 KMDDFWLLKEIQTWLMRSADFNRLKKKQPPAAAVTLHLGANGF 225

RESULT 8

US-09-106-182-3
Sequence 3, Application US/09106182
Patent No. 6046035

GENERAL INFORMATION:
APPLICANT: Shi, Yangu
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Cardiotrophin-like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF385
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPHONE: 301-309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-182-3

Query Match 9.7%; Score 118.5; DB 3; Length 203;
Best Local Similarity 27.5%; Pred. No. 9.4e-05;
Matches 49; Conservative 26; Mismatches 84; Indels 19; Gaps 6;

QY 40 IQKTYDLTRYLHQLSLAGTLYLNYLGPPFPNEBDFPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAYSHLCTYLRGL 96
DB 27 IQKTYDLTRYLHQLSLAGTLYLNYLGPPFPNEBDFPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAYSHLCTYLRGL 96

QY 97 LNDRLRNLQVNEAYSHLCTYLRGLNROA-----TAELRSLAHFCTSLQGLGSIAGW 151
DB 84 -SERLR--QDAALASALPALIDAVRRRQAEINPRAVRLRSLLEDAARQVRLGAAYETVL 140

QY 152 ATLAGY---PLQPLPGTEPMAAPGPAHSDFLQKMDFWLLKEIQTWLMRSADFNRL 205
DB 141 AALGAAGPVPPEPV-ATSAALFTNSAAGVSAVTLGLHVGGLGGEWVSRTEGDLGQL 197

RESULT 9
US-08-233-609-3
Sequence 3, Application US/08233609

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-019B-2

Query Match
Best Local Similarity 97.5%; Score 1193; DB 1; Length 225;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMALCLCTVIMHLPAVPAALNRGTGPGGPGSIQKTYDLTRYLEHQLRSIAGT 60
DB 1 MDLRAGDSWGMALCLCTVIMHLPAVPAALNRGTGPGGPGSIQKTYDLTRYLEHQLRSIAGT 60
QY 61 YNYLGGPPNEPDFFNPRLGAEITLPRATVNLVWMSLNDRLRLTONYEAVSHLLCYLRGL 120
DB 61 YNYLGGPPNEPDFFNPRLGAEITLPRATVNLVWMSLNDRLRLTONYEAVSHLLCYLRGL 120
QY 121 NQAAATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFIQ 180
DB 121 NQAAATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFIQ 180
QY 181 KMDDFWLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGHGF 225
DB 181 KMDDFWLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGHGF 225

RESULT 5
US-09-106-182-2
Sequence 2, Application US/09106182
Patent No. 6046035
GENERAL INFORMATION:
APPLICANT: Shi, Yangu
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Cardiotrophin-Like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,173
REFERENCE/DOCKET NUMBER: PF385

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-182-2

Query Match
Best Local Similarity 97.5%; Score 1193; DB 3; Length 225;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMALCLCTVIMHLPAVPAALNRGTGPGGPGSIQKTYDLTRYLEHQLRSIAGT 60
DB 1 MDLRAGDSWGMALCLCTVIMHLPAVPAALNRGTGPGGPGSIQKTYDLTRYLEHQLRSIAGT 60
QY 61 YNYLGGPPNEPDFFNPRLGAEITLPRATVNLVWMSLNDRLRLTONYEAVSHLLCYLRGL 120
DB 61 YNYLGGPPNEPDFFNPRLGAEITLPRATVNLVWMSLNDRLRLTONYEAVSHLLCYLRGL 120
QY 121 NQAAATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFIQ 180
DB 121 NQAAATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFIQ 180
QY 181 KMDDFWLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGHGF 225
DB 181 KMDDFWLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGHGF 225

RESULT 6
US-08-988-819-2
Sequence 2, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-988-819-2

Query Match
Best Local Similarity 97.5%; Score 1193; DB 3; Length 225;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 121 NROAATAEIRSLAHFCTSLQGLSIGVWATLGYPLPQPLGTEPAMAPGPAHSDFLQ 180
Qy 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225
Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225

RESULT 2

US-08-988-819-5
; Sequence 5, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-988-819-5

Query Match 100.0%; Score 1224; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 8.3e-123;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLRAGDSWGMACICTYLMHLPAVPALNRTGDPGPGPSIQTYDLTRYLEHQRLSLAGT 60
Db 1 MDLRAGDSWGMACICTYLMHLPAVPALNRTGDPGPGPSIQTYDLTRYLEHQRLSLAGT 60
Qy 61 YLNYIGPPNEPDPFNPRLGAETLPRAVTNLEWRSINDRLRLTONYEAYSHLLCYLRGL 120
Db 61 YLNYIGPPNEPDPFNPRLGAETLPRAVTNLEWRSINDRLRLTONYEAYSHLLCYLRGL 120
Qy 121 NROAATAEIRSLAHFCTSLQGLSIGVWATLGYPLPQPLGTEPAMAPGPAHSDFLQ 180
Db 121 NROAATAEIRSLAHFCTSLQGLSIGVWATLGYPLPQPLGTEPAMAPGPAHSDFLQ 180
Qy 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225
Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225

RESULT 3

US-09-016-534-5
; Sequence 5, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI

APPLICANT: ELLIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-534-5

Query Match 100.0%; Score 1224; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 8.3e-123;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLRAGDSWGMACICTYLMHLPAVPALNRTGDPGPGPSIQTYDLTRYLEHQRLSLAGT 60
Db 1 MDLRAGDSWGMACICTYLMHLPAVPALNRTGDPGPGPSIQTYDLTRYLEHQRLSLAGT 60
Qy 61 YLNYIGPPNEPDPFNPRLGAETLPRAVTNLEWRSINDRLRLTONYEAYSHLLCYLRGL 120
Db 61 YLNYIGPPNEPDPFNPRLGAETLPRAVTNLEWRSINDRLRLTONYEAYSHLLCYLRGL 120
Qy 121 NROAATAEIRSLAHFCTSLQGLSIGVWATLGYPLPQPLGTEPAMAPGPAHSDFLQ 180
Db 121 NROAATAEIRSLAHFCTSLQGLSIGVWATLGYPLPQPLGTEPAMAPGPAHSDFLQ 180
Qy 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225
Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225

RESULT 4

US-08-792-019B-2
; Sequence 2, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:

QY 482 CGACGTAGCTGGCCCACTTCTGTACAGACCTCCAGGAGCTGCTGGGAGCATTTGCAAGT 541
DB 561 CCGCGGAGCTGGCCCACTTCTGTACAGACCTCCAGGAGCTGCTGGGAGCATTTGCAAGT 620
QY 542 GTTCATGGGAGCTGGCTTGTGCTTACCACTGCTGGGAGCTGCTGGGAGCTGCTGGGAG 601
DB 621 GTTCATGGGAGCTGGCTTGTGCTTACCACTGCTGGGAGCTGCTGGGAGCTGCTGGGAG 680
QY 602 GCGCCCTGGGAGCTGGCTTGTGCTTACCACTGCTGGGAGCTGCTGGGAGCTGCTGGGAG 661
DB 681 ACTCTGGGAGCTGGCTTGTGCTTACCACTGCTGGGAGCTGCTGGGAGCTGCTGGGAG 740
QY 662 GAGCTTCAGACCTGGCTTGTGCTTACCACTGCTGGGAGCTGCTGGGAGCTGCTGGGAG 721
DB 741 GAGCTTCAGACCTGGCTTGTGCTTACCACTGCTGGGAGCTGCTGGGAGCTGCTGGGAG 800
QY 722 CAGCTTCAGACCTGGCTTGTGCTTACCACTGCTGGGAGCTGCTGGGAGCTGCTGGGAG 781
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QY 782 CT 783
DB 861 TT 862

RESULT 5
AR002595
LOCUS AR002595 797 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 1 from patent US 5741772.
ACCESSION AR002595
VERSION AR002595.1 GI:3964149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 797)
AUTHORS Chang, M.-B.
TITLE Neurotrophic factor NNT-1
JOURNAL Patent: US 5741772-A 1 21-APR-1998;
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source location/Qualifiers
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BASE COUNT 139 a 297 c 218 g 143 t

Query Match 81.7%; Score 669.4; DB 6; Length 797;
Best Local Similarity 92.0%; Pred. No. 4.4e-144;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 5 ATTTAAAGCTTTCGCGGAGCGCGGCTGCGCTCCCACTCCGCGAGCTTGGGAGAGAG 64
DB 1 ATTTAAAGCTTTCGCGGAGCGCGGCTGCGCTCCCACTCCGCGAGCTTGGGAGAGAG 60
QY 65 CCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 124
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DB 120 ATGTAGCTTGTGCTATGCAAGGTGTGTGCACTTCCCTGAGTGCACTCTTATCCG 179
QY 185 ACAGGAGATTCAGGCGCTGGCGCTGCTCATTCAGAAAACCTATGACTCAACCGCTAC 244
DB 180 ACAGGAGATTCAGGCGCTGGCGCTGCTCATTCAGAAAACCTATGACTCAACCGCTAC 239
QY 245 GAGCATCACTCCGAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 304
DB 240 GAGCATCACTCCGAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 299
QY 305 GAGCTGACTTCAATCTCTCTGCACTGGGGGAGAACTCTGCTCCAGGGCAAGCTCAAC 364
DB 300 GAGCTGACTTCAATCTCTCTGCACTGGGGGAGAACTCTGCTCCAGGGCAAGCTCTTAC 359

QY 365 TTGGAAGTGTGGGAGGAGCTCAATGACAGAGCTGCGGCTGACCCAGAACTATGAGGCGTAC 424
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QY 485 CGTACCTGGGCGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 544
DB 480 CGTACCTGGGCGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 539
QY 545 ATGGGAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 604
DB 540 ATGGGAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 599
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QY 665 CTGCAAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 724
DB 660 CTGCAAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 719
QY 725 CTTGGCCCTGGCCCAAGTGAATCTTCTGCAAGATGATGATGATGATGATGATGATGATG 783
DB 720 CTTGGCCCTGGCCCAAGTGAATCTTCTGCAAGATGATGATGATGATGATGATGATGATG 778

RESULT 7
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LOCUS AX392086 797 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 1 from Patent WO0215977.
ACCESSION AX392086
VERSION AX392086.1 GI:19700574
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Senaldi, G.
TITLE Method and compositions for treating ige-related disease using m
JOURNAL t-1 inhibitors
Patent: WO 0215977-A 1 28-FEB-2002;
FEATURES
source location/Qualifiers
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HLGANGP"

BASE COUNT 139 a 297 c 218 g 143 t

Query Match 81.7%; Score 669.4; DB 6; Length 797;
Best Local Similarity 92.0%; Pred. No. 4.4e-144;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 5 ATTTAAAGCTTTCGCGGAGCGCGGCTGCGCTCCCACTCCGCGAGCTTGGGAGAGAG 64

Db 1 ATTTAAAGCTTCGCGGAGCGCGGCTCGCCCTCCCACTCCGCGAGCTTCGCGAGAGAG 60
 Qy 65 CCGCGCCCG 124
 Db 61 CCGGACCG 119
 Qy 125 ATGTTAGCTTGGCTATGACGCGGTCTGTGGCACTTCCCTGCGAGTCCAGCTCTTAATGCG 184
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 Qy 165 AAGAGAGATCCAGCG 244
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 Qy 245 GAGCATCACTCCGAGCTTATGAGTGGAGCTTCACTGAACTAAGTGGGCGCGCGCGCGCG 304
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 Qy 665 CTGAGAGCTTGGCTTACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724
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 Qy 725 CTTGAGAGCTTGGCTTACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 783
 Db 720 CTTGAGAGCTTGGCTTACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 778

RESULT 8
 LOCUS AF176911 797 bp mRNA linear PRI 04-OCT-1999
 DEFINITION Homo sapiens neurotrophin-1/B-cell stimulating factor-3 mRNA,
 complete cds.
 ACCESSION AF176911
 VERSION AF176911.1 GI:6007640
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 797)
 Senaldi, G., Varnum, B.C., Sarmiento, U., Lile, J.,
 Scully, S., Guo, J., Elliott, G., McNinch, J., Shalke, C.L.,
 Freeman, D., Mann, F., Simonet, W.S., Boone, T. and Chang, M.S.
 Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
 IL-6 family
 Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)

JOURNAL
 MEDLINE 99432254
 PUBMED 10500198
 REFERENCE 2 (bases 1 to 797)

AUTHORS Senaldi, G., Varnum, B., Sarmiento, U., Lile, J., Starnes, C.,
 Scully, S., Guo, J., Elliott, G., McNinch, J., Freeman, D., Shalke, C.,
 Mann, F., Simonet, W.S., Boone, T. and Chang, M.S.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive,
 Thousand Oaks, CA 91320, USA
 FEATURES
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 /organism="Homo sapiens"
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 HLGAGR"

BASE COUNT 139 a 297 c 218 g 143 t
 ORIGIN

Query Match 81.7%; Score 669.4; DB 9; Length 797;
 Best Local Similarity 92.0%; Pred. No. 4.4e-144;
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

Qy 5 ATTTAAAGCTTGGCGGAGCGCGGCTCGCCCTCCCACTCCGCGAGCTTCGCGAGAGAG 64
 Db 1 ATTTAAAGCTTGGCGGAGCGCGGCTCGCCCTCCCACTCCGCGAGAGAGAG 60
 Qy 65 CCGCGCCCG 124
 Db 61 CCGGACCG 119
 Qy 125 ATGTTAGCTTGGCTATGACGCGGTCTGTGGCACTTCCCTGCGAGTCCAGCTCTTAATGCG 184
 Db 120 ATGTTAGCTTGGCTGTGCAACGCGGTCTGTGGCACTTCCCTGCGAGTCCAGCTCTTAATGCG 179
 Qy 165 AAGAGAGATCCAGCG 244
 Db 180 AAGAGAGATCCAGCG 239
 Qy 245 GAGCATCACTCCGAGCTTATGAGTGGAGCTTCACTGAACTAAGTGGGCGCGCGCGCGCG 304
 Db 240 GAGCATCACTCCGAGCTTATGAGTGGAGCTTCACTGAACTAAGTGGGCGCGCGCGCGCG 299
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 Db 300 GAGCGAGACTTCAACCTCTCCGCGCTGGGGGCGAGAGACTTGGCCGAGGCGCGCGCGCG 359
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 Db 360 TTGGAAGCTTGGCGGAAAGCTCAATGACAGAGCTGGCGCTGACCCAGAACTATAGCGCTAC 419
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 Db 420 AGTCACTCTCTGTTACTTGTGGTGGCTCAACCGCTGAGGCTGCGCAAGCTGAACTCGGC 479
 Qy 485 CGTACCTTGGCG 544
 Db 480 CGTACCTTGGCG 539
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 Qy 605 CTTGCG 664
 Db 600 CTTGCG 659
 Qy 665 CTGAGAGCTTGGCTTACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724

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Db 660 CTGCAGACCTGGCTGTGGGCTGGCCAGGACTTCAACCGGCTCAAGAAAGATGACG 719
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Qy 725 CCTCCAGCAGCTTCACTCACTTGCAGCTTGAAGGCAATGTTCTTGCAGCTTGCACCT 783
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Db 720 CCTCCAGCAGCTTCACTCACTTGCAGCTTGAAGGCAATGTTCTTGCAGCTTGCACCT 778
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RESULT 9
BC012939 1736 bp mRNA 11nuc PRI 22-AUG-2001
LOCUS
DEFINITION
Homo sapiens, similar to cardiotrophin-1-like cytokine;
neurotrophin-1/B-cell stimulating factor-3, clone MGC:21195
IMAGE:4453813, mRNA, complete cds.
BC012939
ACCESSION BC012939.1 GI:15277894
VERSION
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1736)
Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
REMARK
COMMENT Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalobcm.tmc.edu
Villalon, D.K., Luna, R.A., Hale, S.M., Huylk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
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This clone was selected for full length sequencing because it
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Location/Qualifiers
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BASE COUNT 371 a 546 c 454 g 365 t
ORIGIN
Query Match 79.9%; Score 654; DB 9; Length 1736;

Best Local Similarity 92.0%; Pred. No. 1.4e-140;
Matches 701; Conservative 0; Mismatches 60; Indels 1; Gaps 1;
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Qy 82 GCCGCCAGGCCCAATGAGCTCCGAGGAGGAGGAGCTGAGGAGGAGGAGGAGGAG 141
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Qy 502 CTGAGCTGAGGAGCTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 561
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Db 480 CTGAGCTGAGGAGCTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 539
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Db 660 GGGTTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 719
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LOCUS
DEFINITION
Homo sapiens cardiotrophin-1-like cytokine c1c mRNA, complete cds.
ACCESSION
VERSION AF172854.1 GI:5852980
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1689)
Shi, Y., Wang, W., Yourey, P.A., Gohari, S., Zukauskas, D., Zhang, J.,
Ruden, S., and Alderson, R.F.
REFERENCE Computational EST database analysis identifies a novel member of
the neurotrophic cytokine family
JOURNAL Biochem. Biophys. Res. Commun. 265 (1), 132-138 (1999)

Oy	GAACATATAGAGGGATACAGTCACTCTCTGGTACTTGGGTGGCCCAACCGACAGGCTGC	409
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Db	CAGCATTTCCGGGCGCTCATGCGAGCTCTGGGCTAACCACTGCCCGCCGCGCTGGCGGAC	480
Oy	TGAGCGAGCTGGGGCCCGTGGCCCGCCACAGGTACTTCCCTCCAGAAAGATGGATGACTT	589
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RESULT 12
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 DEFINITION Homo sapiens cardiotrophin-like cytokine (CLC) mRNA, complete cds.
 ACCESSION AY049779
 VERSION AY049779.1 GI:16356642
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 680)
 Hu.X., Xu.Y., Zhang.B., Peng.X., Yuan.J. and Qiang.B.
 Direct Submision
 Submitted (30-JUL-2001) Department of Biochemistry, Institute of
 Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong
 Dan San Tiao, Beijing 100005, P.R. China
 Location/Qualifiers
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Db	601	AGGACTTCAACCGGCTCAAGAAAGAGATGACAGCTCTCAGACAGCTCAGTCAACCTGACACC	660
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Db	661	TGGAGGCAATGATTTCTGA 680	

RESULT 13	AC109138	269155 bp	DNA	linear	ROD 20-MAY-2000
LOCUS	AC109138				
DEFINITION	Mus musculus, clone RP23-41B18, complete sequence.				
ACCESSION	AC109138				
VERSION	AC109138.10				
KEYWORDS	HTG.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 269155)				
TITLE	Bitren, B., Nusbaum, C. and Lander, E.				
JOURNAL	Mus. musculus, clone RP23-41B18				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 269155)				
	Bitren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Basteien, V., Boguslavskiy, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeKrellano, K., Dewar, K., Diaz, J. S., Dode, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Girde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,				

*	17750	24465	contig of 6716 bp in length
*	24466	24465	gap of unknown length
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*	33178	33277	gap of unknown length
*	33278	40901	gap of unknown length
*	40902	41001	contig of 7624 bp in length
*	41002	41961	gap of unknown length
*	41962	contig of 7965 bp in length	
*	49867	49066	gap of unknown length
*	49067	62429	contig of 13363 bp in length
*	62430	62529	gap of unknown length
*	62530	77998	contig of 15456 bp in length
*	77999	78098	gap of unknown length
*	78099	103060	contig of unknown length
*	103061	103160	contig of 24962 bp in length
*	103161	127124	contig of 23964 bp in length
*	127125	127124	gap of unknown length
*	127125	185464	contig of 58240 bp in length
*	185465	185564	gap of unknown length
*	185565	230992	contig of 45428 bp in length
*	230993	231092	gap of unknown length
*	231093	302961	contig of 71865 bp in length

FEATURES	Location/Qualifiers
source	1. .302961

[illegible]

Query Match	66.0%	Score 540.8;	DB 2;	Length 302961;
Best Local Similarity	99.6%	Pred. No. 1.1e-114;		
Matches 542;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;

OY	276	ACCGAACTACCTGGGGGCCCCCTTTAAAGAGCTGACTTCAATCTCTCCGACCTGGGGG	335
	87756	AGCTGAATCTACCTGGGGGCCCCCTTTCAACAGGCTGACTTCAATCTCTCGACTGGGGG	87815
OY	336	CAGAAATCTAGCCAGGAGGCCAGGTCAACTTGAAGTGTGGCGCAAGCTCAATGACAGGC	395

Db	87816	CAGAAACTCTGCCACGGGCGCAGGTCAACTTGGAAAGTGGGGAGGCTCAATGACAGGC	878175
QY	396	TGCGGCTGACCCAGAACTATAGAGGCGTACAGTCACCTCTGTGTATCTTGGCGGCTCTCA	455
Db	87876	TGGGGCTGACCCAGAACTATAGAGGCGTACAGTCACCTCTGTGTATCTTGGCGGCTCTCA	879358
QY	456	ACCGTCAGGCTGCGACAGCTGAACCTCCAGAGTACCTGGGCGCCACTCTGTACAGGCTCC	515
Db	87936	ACCGTCAGGCTGCGACAGCTGAACCTCCAGAGTACCTGGGCGCCACTCTGTACAGGCTCC	879936
QY	516	AGGGCCTGCTGGGCGAGATTGCAAGTGTCAATGGCGACGCTTGGCTAACCACTGCGCCACG	575
Db	87996	AGGGCCTGCTGGGCGAGATTGCAAGTGTCAATGGCGACGCTTGGCTAACCACTGCGCCACG	880556
QY	576	CTCTGCCACGGAGCTGAGCCAGCGCTGGGGCCCTGGGCGCCCTGCCACAGTGACTTCTTCAGA	635
Db	88056	CTCTGCCACGGAGCTGAGCCAGCGCTGGGGCCCTGGGCGCCCTGCCACAGTGACTTCTTCAGA	881156
QY	636	AGATGATGACTCTTGTGGCTGCTGAAAGAGCTGCGACGCTGGTATGAGCGCTTACGCCAAG	695
Db	88116	AGATGATGACTCTTGTGGCTGCTGAAAGAGCTGCGACGCTGGTATGAGCGCTTACGCCAAG	881756
QY	696	ACTTCAACCGGCTTATGAAAGAGATGACAGCTCCACAGCTTCAGTCAACCCCGACCTTGG	755
Db	88176	ACTTCAACCGGCTTATGAAAGAGATGACAGCTTCACAGACTTCAGTCAACCCCGACCTTGG	882356
QY	756	AGGCACATGGTTTCTGACCTCTGACCCCTTAAACCCCAACCTTCAGAGGCCAGTCAAGCTGT	815
Db	88236	AGGCACATGGTTTCTGACCTCTGACCCCTTAAACCCCAACCTTCAGAGGCCAGTCAAGCTGT	882936
QY	816	GCCTT 819	
Db	88296	GCCTT 88299	

RESULT 15			
AX205060			
LOCUS	AX205060	1692 bp	DNA
DEFINITION	Sequence 19 from Patent WO0155219.		linear
ACCESSION	AX205060		
VERSION	AX205060.1		
KEYWORDS	GI:15394299		
SOURCE			
ORGANISM	synthetic construct		
	synthetic construct		
	artificial sequences.		
REFERENCE	1		
AUTHORS	Elson,G. and Gauchat,J.F.		
TITLE	Secscntfr/mtc-1 fusion protein		
JOURNAL	Patent: WO 0155219-A 19 02-AUG-2001;		
	PIERRE FABRE MEDICAMENT (FR)		
FEATURES			
source	Location/Qualifiers		
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CDS

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Query Match 62.2%; Score 509.2; DB 6; Length 1692;
Best Local Similarity 91.1%; Pred. No. 4e-107;
Matches 541; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY	176	CTTAATCGCAGAGAGATCCAGGCTGAGCCCTCCATCCAGAAAACCTATGACCTCAC	235
DB	1066	CTCAATCGCAGAGGAGCCAGGGCTGAGCCCTCCATCCAGAAAACCTATGACCTCAC	1125
QY	236	CGCTACCTGAGATCACTCCGACACTAGCTGGAGACTTACCTGAACCTACTGAGGCC	295
DB	1126	CGCTACCTGAGAGCACCACCTCCGACACTTGGCTGGAGACTATCTGAACCTACTGAGGCC	1185
QY	296	CCCTTCAAGAGGCTGACTTCAATCTCTCGACTGGGGGCAAGAACTGCGCCAGGGCC	355
DB	1186	CTTTTCAAGAGGCTGACTTCAACCTCTCCGCTGGGGGCAAGAACTGCGCCAGGGCC	1245
QY	356	ACGGTCACCTGGAAGTGTGGCGAAGCTCAATGACAGGCTGGGCTGACCCGAACTAT	415
DB	1246	ACTGTTGACTTGGAGGTGTGGGAAGCTCAATGACAACTGGGCTGACCCGAACTAC	1305
QY	416	GAGGCTTACATGACCTCTGTGTACTTGGCGTGGCTCAACCTCAGGCTGCACAGCT	475
DB	1306	GAGGCTTACAGGCACCTCTGTGTACTTGGCGTGGCTCAACCTCAGGCTGCACAGCT	1365
QY	476	GAATCCGACGTAGCTGAGCCCACTTCTGACAGGCTCGAGGGCTGCTGGGCAAGCAT	535
DB	1366	GAGCTGCGCGGAGCTTGGCCCACTTCTGACAGGCTCGAGGGCTGCTGGGCAAGCAT	1425
QY	536	GCAGGTGTCATGCGCAGCTTGGCTACCACTGCCCCAGCCTTGCACAGGGACTGAGCCA	595
DB	1426	GCGGGGCTCATGGCACTTGGGCTACCACTGCCCCAGCCTTGCACAGGGACTGAGCCA	1485
QY	596	GCCTGGGCCCCCTGGCCCTGCCCCACAGTACTTCTCCAGAAATGATGACTTCTGGCTG	655
DB	1486	ACTTGGACTCTGGCCCTGCCCCACAGTACTTCTCCAGAAATGATGACTTCTGGCTG	1545
QY	656	CTGAAGGAGCTGAGACTGGCTATGGCTTACGCAAGGACTTCAACCGGCTTAAGAAG	715
DB	1546	CTGAAGGAGCTGAGACTGGCTATGGCTTACGCAAGGACTTCAACCGGCTTAAGAAG	1605
QY	716	AAGATGACAGCTTCCAGCAGCTTCAGTCAACCTGCACTTGGAGGACATGTTTC	769
DB	1606	AAGATGACAGCTTCCAGCAGCTTCAGTCAACCTGCACTTGGAGGACATGTTTC	1659

Search completed: February 9, 2004, 08:01:33
Job time : 3292.64 secs

END
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OM protein - protein search, using SW model

Run on: February 9, 2004, 06:14:57 ; Search time 35.5 Seconds
(without alignments)
1006.013 Million cell updates/sec

Title: US-09-931-704-2
Perfect score: 1226
Sequence: 1 MDLRAGDSWGMIACTLVLM.....KKMQPAAAVTLHGAGGF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1226	100.0	225	19	AAW29715
2	1226	100.0	225	19	AAW56141
3	1226	100.0	225	20	AAW94466
4	1226	100.0	225	21	AAW87813
5	1226	100.0	225	22	AAW63543
6	1226	100.0	225	23	AAU78176
7	1226	100.0	225	23	AAW25831
8	1214	99.0	223	22	AAE00828
9	1204	98.2	321	22	ABW11896

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11	1197	97.6	260	22	AAW78415
12	1193	97.3	225	19	AAW29715
13	1193	97.3	225	19	AAW56142
14	1193	97.3	225	21	AAW87814
15	1193	97.3	225	23	AAW78177
16	1169	95.4	215	21	AAW19586
17	1136	92.7	215	21	AAW19587
18	885	72.2	164	22	ABG55577
19	885	72.2	164	22	ABW40317
20	885	72.2	164	22	ABW24716
21	885	72.2	164	22	AAW61118
22	885	72.2	164	22	AAW73827
23	885	72.2	164	22	AAW20115
24	885	72.2	164	22	AAW34012
25	885	72.2	164	23	ABG43716
26	162.5	13.3	208	20	AAW09197
27	160	13.1	208	20	AAW09196
28	118.5	9.7	203	16	AAW83965
29	118.5	9.7	203	17	AAW88204
30	118.5	9.7	203	18	AAW29237
31	96.5	7.9	243	22	AAW09153
32	96.5	7.9	243	22	AAW20277
33	96.5	7.9	243	23	ABG32291
34	96.5	7.9	243	23	AAU76375
35	96.5	7.9	243	24	ABG75877
36	93	7.6	419	24	ABU2010
37	92	7.5	332	21	AAW22132
38	92	7.5	332	21	AAW40321
39	91.5	7.5	201	16	AAW83967
40	91.5	7.5	201	18	AAW29238
41	91.5	7.5	201	20	AAW06490
42	91.5	7.5	201	21	AAW27652
43	91.5	7.5	201	21	AAW31004
44	91.5	7.5	201	21	AAW93697
45	91.5	7.5	201	21	AAW87818

ALIGNMENTS

RESULT 1					
ID	AAW29715	standard; Protein; 225 AA.			
XX	AAW29715;				
AC	AAW29715;				
XX	AAW29715;				
DT	09-NOV-1998	(first entry)			
XX	09-NOV-1998				
DE	Human neurotrophic factor NNT-1.				
XX	NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;				
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease;				
KW	amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;				
KW	peripheral neuropathy; dysreflexia; neural retina degeneration;				
KW	common variable immunodeficiency; CVID; selective iga deficiency;				
KW	hypogammaglobulinemia; X-linked agammaglobulinemia; antiseptic;				
XX	therapy.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	Peptide	1..27			
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XX		28..225			
XX		/label= Mat_protein			
XX	MO9833922-A1.				
XX	06-AUG-1998.				
PD	02-FEB-1998;	98WO-US02363.			
XX					

Human protein SEQ
Human protein SEQ
Mouse neurotrophic
Amino acid sequenc
Murine NNT-1 prote
Human novel neurot
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Mouse interleukin-
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Human interleukin
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M. echinospora cal
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Human cardiotroph

PR 30-JAN-1998; 98US-0016534.
 PR 03-FEB-1997; 97US-0792019.
 (AMGE-) AMGEN INC.
 PI Chang M, Elliot GS, Sarmiento U, Senaldi G;
 DR WPI; 1998-437475/37.
 DR N-PSDB; AAV47510, AAV47511.

PT Newly isolated nucleic acid encoding human or murine neurotrophic
 factor NNT-1 - useful for treatment of neurological and
 immunological diseases or inflammation, also as vaccine adjuvant

PS Claim 12; Fig 3; 120pp; English.

CC This is the amino acid sequence of a novel neurotrophic factor,
 CC designated NNT-1, that is a growth factor for neurons and for B or
 CC T cells. It was deduced from isolated cDNA (see AAV47510) and
 CC genomic DNA (see AAV47511) clones. Vectors containing the cDNA or
 CC genomic DNA and host cells are provided for use in the production
 CC of NNT-1 polypeptides. These are used to treat: (i) neurological
 CC or immunological diseases, specifically Alzheimer's, Parkinson's
 CC or Huntington's diseases, amyotrophic lateral sclerosis,
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
 CC degeneration of the neural retina, or conditions characterised by T
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),
 CC selective IGA deficiency, hypogammaglobulinemia and X-linked
 CC agammaglobulinemia (claimed), but many others disclosed; and (ii)
 CC inflammation. NNT-1 is also able to boost immunoreactivity and
 CC antibody production following vaccination, and, since it inhibits
 CC tumour necrosis factor production, it may also be useful for
 CC treating sepsis. In addition, cells that have been engineered to
 CC express NNT-1 can be implanted, or nucleic acids are delivered in
 CC gene therapy vectors.

XX Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 19; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.6e-118;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMALACTCTVLMHLPVAVPALNRTGDPGPGPSIOKTYDITRYLHQLRSLAGT 60
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 DB 181 KMDDFWLKELQITWLMRSKADFNRLKKMQPPAAVTLHLGAHGF 225

RESULT 2
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 ID AAW56141 standard; Protein; 225 AA.
 XX AAW56141;

DT 13-JUL-1998 (first entry)

XX Amino acid sequence of human neurotrophic factor NNT-1.

DE Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
 XX treatment; neurological disease; degeneration; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.
 XX

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /note= "signal peptide"
 FT Protein 28..225
 FT /note= "mature protein"

PN US5741772-A.
 XX 21-APR-1998.

XX 03-FEB-1997; 97US-0792019.

XX 03-FEB-1997; 97US-0792019.

PA (AMGE-) AMGEN INC.

PI Chang M;

DR WPI; 1998-260526/23.

DR N-PSDB; AAV22652.

PT Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
 useful for stimulating growth of motor and sympathetic neurons

PS Claim 1; Fig 3; 41pp; English.

CC The present sequence represents a human neurotrophic factor, designated
 CC NNT-1, which is capable of stimulating growth of motor or sympathetic
 CC neurons. The NNT-1 protein is useful in the treatment of neurological
 CC diseases characterised by the degeneration and death of particular
 CC classes of neurons. These diseases specifically include Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC stroke and various degenerative disorders affecting vision.

XX Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 19; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.6e-118;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 181 KMDDFWLKELQITWLMRSKADFNRLKKMQPPAAVTLHLGAHGF 225

RESULT 3
 AAW94466
 ID AAW94466 standard; Protein; 225 AA.
 XX AAW94466;

DT 22-APR-1999 (first entry)

XX Human cardiostrophin-like cytokine protein.

DE Human; cardiostrophin-like cytokine; interleukin 6 cytokine family;
 XX CLC; IL-6; diagnosis; detection; immune system-related disorder;
 KW cancer; cardiac disorder; heart failure; hypertension; cancer;
 XX autoimmune disorder; infection.

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XX FT Peptide
XX FT 1..27
XX FT /label= signal
XX FT 28..225
XX FT /label= Cardiotrophin-like_cytokine
XX FT Domain
XX FT 74..79
XX FT /label= CD-1
XX FT /note= "conserved domain"
XX FT 150..156
XX FT /label= CD-11
XX FT /note= "conserved domain"
XX FT 194..198
XX FT /label= CD-111
XX FT /note= "conserved domain"
XX PN WO9900415-A1.
XX PD 07-JAN-1999.
XX XX
XX PF 29-JUN-1998; 98WO-US13129.
XX XX
XX PR 30-JUN-1997; 97US-0051311.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Ruben SM, Shi Y;
XX DR WPI; 1999-095678/08.
XX DR N-PSDB; AAX16161.
XX PT New isolated cardiotrophin-like cytokine nucleic acid - used to
XX PT develop products for treating cardiac and immune system disorders,
XX PT e.g. heart failure, hypertension, cancers, autoimmune disorders and
XX PT infections
XX PS Claim 1; Fig 1; 103pp; English.
XX CC The present invention relates to a novel cardiotrophin-like cytokine
XX CC (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine
XX CC family. The present sequence represents the human CLC protein. The
XX CC present invention also describes screening methods for identifying
XX CC agonists and antagonists of CLC activity, as well as methods for
XX CC detecting cardiac and immune system-related disorders and
XX CC therapeutic methods for treating cardiac and immune system-related
XX CC disorders, e.g heart failure, hypertension, cancers, autoimmune
XX CC disorders and infections.
XX SO Sequence 225 AA:
XX
XX Query Match 100.0%; Score 1226; DB 20; Length 225;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-118;
XX Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 MDLRADDSWGMACLCCTVLMHLPAVPALNRTGDPGPGPSIOKTYDITRYLHQLSLAGT 60
XX DB 1 MDLRADDSWGMACLCCTVLMHLPAVPALNRTGDPGPGPSIOKTYDITRYLHQLSLAGT 60
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XX DB 61 YLNYLGPPFNPPDPNPRPGAETLPRAATVDLEWVRSNLNDKRLTONYEAVSHLLCYLRGL 120
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XX FT 28..225
XX FT /label= Cardiotrophin-like_cytokine
XX FT Domain
XX FT 74..79
XX FT /label= CD-1
XX FT /note= "conserved domain"
XX FT 150..156
XX FT /label= CD-11
XX FT /note= "conserved domain"
XX FT 194..198
XX FT /label= CD-111
XX FT /note= "conserved domain"
XX PN WO9900415-A1.
XX PD 07-JAN-1999.
XX XX
XX PF 29-JUN-1998; 98WO-US13129.
XX XX
XX PR 30-JUN-1997; 97US-0051311.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Ruben SM, Shi Y;
XX DR WPI; 1999-095678/08.
XX DR N-PSDB; AAX16161.
XX PT New isolated cardiotrophin-like cytokine nucleic acid - used to
XX PT develop products for treating cardiac and immune system disorders,
XX PT e.g. heart failure, hypertension, cancers, autoimmune disorders and
XX PT infections
XX PS Claim 1; Fig 1; 103pp; English.
XX CC The present invention relates to a novel cardiotrophin-like cytokine
XX CC (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine
XX CC family. The present sequence represents the human CLC protein. The
XX CC present invention also describes screening methods for identifying
XX CC agonists and antagonists of CLC activity, as well as methods for
XX CC detecting cardiac and immune system-related disorders and
XX CC therapeutic methods for treating cardiac and immune system-related
XX CC disorders, e.g heart failure, hypertension, cancers, autoimmune
XX CC disorders and infections.
XX SO Sequence 225 AA:
XX
XX Query Match 100.0%; Score 1226; DB 21; Length 225;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-118;
XX Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MDLRADDSWGMACLCCTVLMHLPAVPALNRTGDPGPGPSIOKTYDITRYLHQLSLAGT 60
XX DB 1 MDLRADDSWGMACLCCTVLMHLPAVPALNRTGDPGPGPSIOKTYDITRYLHQLSLAGT 60
XX QY 61 YLNYLGPPFNPPDPNPRPGAETLPRAATVDLEWVRSNLNDKRLTONYEAVSHLLCYLRGL 120
XX DB 61 YLNYLGPPFNPPDPNPRPGAETLPRAATVDLEWVRSNLNDKRLTONYEAVSHLLCYLRGL 120
```

Db 61 YLNTYLGPPNPDNPRLGAETLPRAVTDLEWRSINDKRLTONYEAYSHLCTYRGL 120
Qy 121 NRQATAEIARRSLAHFCTSLQGLGSIAGWMAALGYPLPPLPGTEPTTPGPASDFLQ 180
Db 121 NRQATAEIARRSLAHFCTSLQGLGSIAGWMAALGYPLPPLPGTEPTTPGPASDFLQ 180
Qy 181 KMDDFWLKEIQTWLMRSAKDPNRLKKMQPPAAAVTLHLGAHGF 225
Db 181 KMDDFWLKEIQTWLMRSAKDPNRLKKMQPPAAAVTLHLGAHGF 225

RESULT 5
AAG63543
ID AAG63543 standard; Protein; 225 AA.
AC AAG63543;
XX
XX
DT 15-OCT-2001 (first entry)
XX
XX Amino acid sequence of a human NNT-1 protein.
DE
XX NNT-1; SCNTRAlpha; nervous system; neuron; nervous system;
XX neuro-muscular function; tumour; immune system; haematopoietic system;
XX reproductive system; liver; skeletal muscle; neurodegenerative disease;
XX amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;
XX muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
XX blastocyst implantation; thrombosis; retinal disease;
XX retinal pigmentosis.
XX
XX Homo sapiens.
OS
XX
XX WO200155172-A2.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 26-JAN-2001; 2001WO-FR00253.
PF
XX
XX 27-JAN-2000; 2000FR-0001035.
PR
XX 12-OCT-2000; 2000FR-0013089.
XX
XX (FABR) FABRE MEDICAMENT SA PIERRE.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA
XX
XX Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H,
PI
XX MPI: 2001-488773/53.
XX
XX N-PSDB; AAH74484.
DR
XX
XX A complex comprising a NNT-1 protein and a CLF-1 and/or SCNTRAlpha
PT protein useful to treat neurodegenerative disease including Parkinson's
PT and Huntington's, obesity and cancer -
XX
XX Claim 2, Page 58; 67pp; French.
PS
XX
XX The present sequence represents a human NNT-1 protein. The specification
CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or
CC SCNTRAlpha protein. The NNT-1/CLF-1 complex is used to modulate
CC activity of the SCNTRAlpha/gp130/LiFbeta receptor complex, or to
CC induce phosphorylation of the tyrosine of gp130 and LiFbeta,
CC particularly where cells expressing the receptor complex are in the
CC central or peripheral nervous system, in neurons implicated in
CC neuro-muscular function or in skeletal muscle. The complex or
CC antibodies are also used to decrease the survival, growth or
CC proliferation of tumour cells or to facilitate the proliferation and/or
CC inhibit differentiation of cells stocks. The complex is also used to
CC modulate activity of the gp130/LiFbeta receptor or cells expressing
CC that receptor, particularly those cells implicated in the immune,
CC haematopoietic, nervous or reproductive system, the liver or skeletal
CC muscle. Molecules of the invention may be used to prevent or treat
CC neurodegenerative diseases including amyotrophic lateral sclerosis,
CC Parkinson's and Huntington's disease, to repair or regenerate nervous
CC or muscular tissue or to maintain muscular mass in paralysis patients.
CC They may also be used to treat cancer, obesity and associated diseases.

CC and to improve fertility, particularly to avoid endometriosis and/or
CC assist blastocyst implantation, thrombosis, or retinal disease,
CC particular retinal pigmentosis.
XX
XX Sequence 225 AA;
SQ
Query Match 100.0%; Score 1226; DB 22; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-118;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLRAGDSWGMALACTCTYLWHLPAVPALNRTGDPGPGPSIOCTYDLTRYLHQLSLAGT 60
Db 1 MDLRAGDSWGMALACTCTYLWHLPAVPALNRTGDPGPGPSIOCTYDLTRYLHQLSLAGT 60
Qy 61 YLNTYLGPPNPDNPRLGAETLPRAVTDLEWRSINDKRLTONYEAYSHLCTYRGL 120
Db 61 YLNTYLGPPNPDNPRLGAETLPRAVTDLEWRSINDKRLTONYEAYSHLCTYRGL 120
Qy 121 NRQATAEIARRSLAHFCTSLQGLGSIAGWMAALGYPLPPLPGTEPTTPGPASDFLQ 180
Db 121 NRQATAEIARRSLAHFCTSLQGLGSIAGWMAALGYPLPPLPGTEPTTPGPASDFLQ 180
Qy 181 KMDDFWLKEIQTWLMRSAKDPNRLKKMQPPAAAVTLHLGAHGF 225
Db 181 KMDDFWLKEIQTWLMRSAKDPNRLKKMQPPAAAVTLHLGAHGF 225

RESULT 6
AAU78176
ID AAU78176 standard; Protein; 225 AA.
XX
XX AAU78176;
AC
XX
XX 05-JUN-2002 (first entry)
DT
XX
XX Human novel neurotrophic factor NNT1.
DE
XX
XX Human; NNT1; neurotrophic factor; IGF-related disease;
XX Type I allergic disease; allergic rhinitis; eczema; dermatitis;
XX pollinosis; asthma; immune disease; cancer; arteriosclerosis;
XX vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
XX inflammatory arthritis; osteoarthritis; inflammatory joint disease;
XX autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
XX inflammatory bowel disease; transplant rejection; reproductive disorder;
XX graft versus host disease; infertility; miscarriage; preterm labour.
XX
XX Homo sapiens.
OS
XX
XX WO200215977-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US25906.
PF
XX
XX 18-AUG-2000; 2000US-226436P.
PR
XX 16-AUG-2001; 2001US-0931704.
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Senaldi G;
PI
XX
XX MPI: 2002-280867/32.
XX
XX N-PSDB; ABK11647.
DR
XX
XX Treating Immunoglobulin E-related disease, modulating IGE levels in a
PT patient, preventing IGF-related disease and treating allergic diseases,
PT involves administering NNT-1 inhibitor to a patient -
XX
XX Claim 2; Fig 3; 63pp; English.
PS
XX
XX The invention relates to treating Immunoglobulin E (IGE)-related disease,
CC modulating IGE levels in a patient, preventing an IGE-related disease,
CC and treating allergic diseases, comprising administering a

CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
CC inhibitor to a patient. Also included are a method of diagnosing an
CC IGF-related disease or susceptibility to an IGF-related disease, by
CC determining the presence or amount of expression of an NNT polypeptide
CC encoded by a NNT nucleotide sequence, its fragment or naturally
CC occurring variant, and diagnosing an IGF-related disease or
CC susceptibility of an IGF-related disease based on the presence or amount
CC of expression of the polypeptide and a pharmaceutical composition for use
CC in treating IGF-related disease, comprising the NNT inhibitor.
CC The NNT inhibitor is useful for preventing and treating IGF-related
CC disease, modulating IGF levels, and treating allergic diseases e.g.
CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,
CC pollinosis, asthma, immune diseases and disorders, diseases involving
CC abnormal cell proliferation including cancer, arteriosclerosis and
CC vascular restenosis, diseases and conditions relating to dysfunction of
CC immune system including rheumatoid arthritis, psoriatic arthritis,
CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,
CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
CC bowel disease, transplant rejection, and graft versus host disease, and
CC reproductive diseases and disorders including infertility, miscarriage,
CC preterm labour and delivery, and endometriosis. The present sequence
CC represents human NNT1.

XX Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 23; Length 225;

Best Local Similarity 100.0%; Pred. No. 1,6e-118; Mismatches 0; Gaps 0;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMALACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDTRYLEHQSLACT 60

Db 1 MDLRAGDSWGMALACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDTRYLEHQSLACT 60

QY 61 YNYLGGPPNEDPFPNPRIGAEITLPRATYDLEWMSLNDKRLTONYEYSHLCTLRGL 120

Db 61 YNYLGGPPNEDPFPNPRIGAEITLPRATYDLEWMSLNDKRLTONYEYSHLCTLRGL 120

QY 121 NNOAATAEIRSRSAHCTSLQGLSIGVMAALGYPLPQPLPGTEPTTPGPAHSDFLQ 180

Db 121 NNOAATAEIRSRSAHCTSLQGLSIGVMAALGYPLPQPLPGTEPTTPGPAHSDFLQ 180

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

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QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAATVTLHGANGF 225

</

XX 02-JUL-2001 (first entry)
DT Human cardiotrophin-like cytokine (CLC) protein.
XX
DE Human cardiotrophin-like cytokine (CLC) protein.
XX
XX Human, biologically active complex; haemopoietin receptor; NRG;
KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
XX differentiation; cell survival; neurotrophic activity.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /label= signal_peptide
FT 28..223
FT Protein /label= Human mature CLC protein
FT /note= "Cardiotrophin-like cytokine"
XX
XX WO200127157-A1.
XX
XX 19-APR-2001.
XX
XX 06-OCT-2000; 2000WO-AU01216.
XX
XX 08-OCT-1999; 99AU-0003327.
XX
XX 12-MAY-2000; 2000AU-0007489.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
PI Nakata Y, Haesegawa M;
XX
XX WPI; 2001-281978/29.
XX
XX N-PSDB; AAD04201.
XX
XX New biologically active complex comprising NRG and
PT cardiotrophin-like cytokine, for facilitating proliferation,
PT differentiation and/or survival of a cell -
XX
XX Claim 32; Page 114-115; 123pp; English.
XX
XX The present invention relates to a biologically active complex comprising
CC a haemopoietin receptor, NRG and cardiotrophin-like cytokine (CLC).
CC The complex is useful in the manufacture of a medicament for the
CC treatment and/or prophylaxis of a subject, as it is involved in
CC facilitating proliferation, differentiation and/or survival of a cell.
CC The complex or its components have neurotrophic activity. The present
CC sequence is human cardiotrophin-like cytokine (CLC) protein.
XX
XX Sequence 223 AA;
SQ

Query Match 99.0%; Score 1214; DB 22; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMALACTVLMHLPAVPALNRTGDPGPGPSIOKTYDLYRLEHQLSLAGT 60
DB 1 MDLRAGDSWGMALACTVLMHLPAVPALNRTGDPGPGPSIOKTYDLYRLEHQLSLAGT 60
QY 61 YINYNGPPNEDPDPNPRIGASTLPRAATVDLEWRSNDKRLTONYEAYSHLCTYRGL 120
DB 61 YINYNGPPNEDPDPNPRIGASTLPRAATVDLEWRSNDKRLTONYEAYSHLCTYRGL 120
QY 121 NROATTAELRRSLAHFCTSLGGLGSIAGWMAALGPPLPQPLRGTEPTWTPGPAHSDFLQ 180
DB 121 NROATTAELRRSLAHFCTSLGGLGSIAGWMAALGPPLPQPLRGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFMLLKEIQTWLMRSKADFNRLKKKQPPAAAVTTLHGLAH 223
DB 181 KMDDFMLLKEIQTWLMRSKADFNRLKKKQPPAAAVTTLHGLAH 223

RESULT 9

ABBI1896
ID ABBI1896 standard; peptide, 321 AA.
XX
XX AC ABBI1896;
XX
XX 11-JAN-2002 (first entry)
DT
DE Human cardiotrophin-like cytokine homologue, SEQ ID NO:2266.
XX
XX
KW Human, cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; anti-inflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antitumor.
XX
XX OS Homo sapiens.
XX
XX WO200157188-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US03800.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560875.
XX
XX (HISE-) HISEQ INC.
XX
XX Tang YT, Liu C, Dymanc RT;
PI
XX
XX WPI; 2001-457740/49.
XX
XX N-PSDB; ABA09140.
XX
XX
XX Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
XX Claim 20; Page 273; 1963pp; English.
XX
XX Sequences ABBI0981-ABBI2330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides,
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, and hence
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemorectic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention.

XX Sequence 321 AA;

Query Match 98.2%; Score 1204; DB 22; Length 321;
Best Local Similarity 99.1%; Pred. No. 5e-116;
Matches 221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LRAGDSMGMLACTCTVLMHLPAVPALNRTGDPGPGPSIOKTYDLTRYLHQLRSLAGTYL 62
DB 99 LPTGDSMGMLACTCTVLMHLPAVPALNRTGDPGPGPSIOKTYDLTRYLHQLRSLAGTYL 158
QY 63 NYLGPPFNEPDPFNPRLGAETLPRAATVDLEWRSINDKRLTONYEAYSHLICYRGLNR 122
DB 159 NYLGPPFNEPDPFNPRLGAETLPRAATVDLEWRSINDKRLTONYEAYSHLICYRGLNR 218
QY 123 QAAATLRRSLAHFCTSIQGLGSIAGWMAALGYPLPQLPCTEPTWTPGPAHSDFLQKM 182
DB 219 QAAATLRRSLAHFCTSIQGLGSIAGWMAALGYPLPQLPCTEPTWTPGPAHSDFLQKM 278
QY 183 DDFWLKELQTLWMSAKDFNRLKKKMPAAAVTLHGAGF 225
DB 279 DDFWLKELQTLWMSAKDFNRLKKKMPAAAVTLHGAGF 321

RESULT 10

AAAT9399
ID AAM79399 standard; Protein; 321 AA.

XX AAM79399;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3045.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

OS WO200157190-A2.

DT 09-AUG-2001.

DE 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.

XX (HYSR-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;

DR WPI; 2001-476283/51.
DR N-PSDB; AAK52532.

XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -

PS Claim 20; Page 237; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK51435) and the
CC encoded polypeptides (AAM79323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.

XX Sequence 321 AA;

Query Match 98.2%; Score 1204; DB 22; Length 321;
Best Local Similarity 99.1%; Pred. No. 5e-116;
Matches 221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LRAGDSMGMLACTCTVLMHLPAVPALNRTGDPGPGPSIOKTYDLTRYLHQLRSLAGTYL 62
DB 99 LPTGDSMGMLACTCTVLMHLPAVPALNRTGDPGPGPSIOKTYDLTRYLHQLRSLAGTYL 158
QY 63 NYLGPPFNEPDPFNPRLGAETLPRAATVDLEWRSINDKRLTONYEAYSHLICYRGLNR 122
DB 159 NYLGPPFNEPDPFNPRLGAETLPRAATVDLEWRSINDKRLTONYEAYSHLICYRGLNR 218
QY 123 QAAATLRRSLAHFCTSIQGLGSIAGWMAALGYPLPQLPCTEPTWTPGPAHSDFLQKM 182
DB 219 QAAATLRRSLAHFCTSIQGLGSIAGWMAALGYPLPQLPCTEPTWTPGPAHSDFLQKM 278
QY 183 DDFWLKELQTLWMSAKDFNRLKKKMPAAAVTLHGAGF 225
DB 279 DDFWLKELQTLWMSAKDFNRLKKKMPAAAVTLHGAGF 321

RESULT 11

AAAT8415
ID AAM78415 standard; Protein; 260 AA.

XX AAM78415;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1077.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

OS WO200157190-A2.

DT 09-AUG-2001.

DE 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HSE-) HSEBQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI: 2001-476283/51.
 DR N-PSDB; AAKS1548.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 3306; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAW80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 CC
 SQ Sequence 260 AA;
 Query Match 97.6%; Score 1197; DB 22; Length 260;
 Best Local Similarity 98.7%; Pred. No. 2e-115;
 Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 LRAAGSWGMLACTCTVWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 62
 DB 38 LRTGSGWGLACTCTVWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 97
 QY 63 NYLGPPFNPDPNPRLGAEITLPRATVDEWRSINDKRLTONYEAYSHLCTYRGLN 122
 DB 98 NYLGPPFNPDPNPRLGAEITLPRATVDEWRSINDKRLTONYEAYSHLCTYRGLN 157
 QY 123 QAATAELRSLAHFCTSLQGLLSIAGVAAALGYPLPQPLPCTEPTWTGPAHSDP 182
 DB 158 QAATAELRSLAHFCTSLQGLLSIAGVAAALGYPLPQPLPCTEPTWTGPAHSDP 217
 QY 183 DDFWLLKELQVTWLRSAKDFNRLKKMKOPPAAVTLHLGAHGF 225
 DB 218 DDFWLLKELQVTWLRSAKDFNRLKKMKOPPAAVTLHLGAHGF 260
 RESULT 12
 AAW29716
 ID AAW29716 standard; Protein; 225 AA.
 XX
 AC AAW29716;
 XX
 DT 09-NOV-1998 (first entry)
 XX
 DE Mouse neurotrophic factor NNT-1.
 XX
 KW NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 KW peripheral neuropathy; dystrophy; neural retina degeneration;
 KW common variable immunodeficiency; CVID; selective IGA deficiency;
 KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;

KW therapy.
 XX
 OS Mus sp.
 XX
 FT Key
 FT Peptide 1..27
 FT Protein /label= Sig_peptide
 FT /label= 28..225
 FT /label= Mat_protein
 PN W09833922-A1.
 PD 06-AUG-1998.
 XX
 PF 02-FEB-1998; 98WO-US02363.
 XX
 PR 30-JAN-1998; 98US-0016534.
 PR 03-FEB-1997; 97US-0792019.
 XX
 PA (AMGE-) AMGEN INC.
 PI Chang M, Elliot GS, Sarmiento U, Senaldi G;
 DR WPI: 1998-437475/37.
 DR N-PSDB; AAV47512.
 XX
 PT Newly isolated nucleic acid encoding human or murine neurotrophic
 PT factor NNT-1 - useful for treatment of neurological and
 PT immunological diseases or inflammation, also as vaccine adjuvant
 XX
 PS Claim 13; Fig 5; 120pp; English.
 XX
 CC This is the amino acid sequence of a murine neurotrophic factor,
 CC designated NNT-1, that is a growth factor for neurons and for B or
 CC T cells. It was deduced from isolated NNT-1 cDNA (see AAV47512).
 CC Human NNT-1 (see AAW29715) is also provided. Vectors and host cells
 CC for use in the production of human murine recombinant NNT-1
 CC polypeptides. These are used to treat: (i) neurological or
 CC immunological diseases, specifically Alzheimer's, Parkinson's
 CC or Huntington's diseases, amyotrophic lateral sclerosis,
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
 CC degeneration of the neural retina, or conditions characterised by T
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),
 CC selective IGA deficiency, hypogammaglobulinaemia and X-linked
 CC agammaglobulinaemia (claimed), but many others disclosed; and (ii)
 CC inflammation. NNT-1 is also able to boost immunoreactivity and
 CC antibody production following vaccination, and, since it inhibits
 CC tumor necrosis factor production, it may also be useful for
 CC treating sepsis. In addition, cells that have been engineered to
 CC express NNT-1 can be implanted, or nucleic acids are delivered in
 CC gene therapy vectors.
 XX
 SQ Sequence 225 AA;
 Query Match 97.3%; Score 1193; DB 19; Length 225;
 Best Local Similarity 96.9%; Pred. No. 4.3e-115;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDLRAGSWGMLACTCTVWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 60
 DB 1 MDLRAGSWGMLACTCTVWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 60
 QY 61 YINYVGPPFNPDPNPRLGAEITLPRATVDEWRSINDKRLTONYEAYSHLCTYRGL 120
 DB 61 YINYVGPPFNPDPNPRLGAEITLPRATVDEWRSINDKRLTONYEAYSHLCTYRGL 120
 QY 121 NROAATAELRSLAHFCTSLQGLLSIAGVAAALGYPLPQPLPCTEPTWTGPAHSDP 180
 DB 121 NROAATAELRSLAHFCTSLQGLLSIAGVAAALGYPLPQPLPCTEPTWTGPAHSDP 180
 QY 181 KMDDFWLLKELQVTWLRSAKDFNRLKKMKOPPAAVTLHLGAHGF 225
 DB 181 KMDDFWLLKELQVTWLRSAKDFNRLKKMKOPPAAVTLHLGAHGF 225

QY 61 YNATGPPFNEPDPRLGAEITLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLRGL 120
DB 61 YNATGPPFNEPDPRLGAEITLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLRGL 120
QY 121 NROAATAEIRSLAHFCTSLQGLGSIAGVMAALGYPPLPGTEPTWTPGPAHSDFLQ 180
DB 121 NROAATAEIRSLAHFCTSLQGLGSIAGVMAALGYPPLPGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKELQTWLMRSKADFNRLKKKQOPPAATVTLHGAHGF 225
DB 181 KMDDFWLKELQTWLMRSKADFNRLKKKQOPPAATVTLHGAHGF 225
RESULT 15
AAU78177.
ID AAU78177 standard; Protein; 225 AA.
AC AAU78177;
XX
XX 05-JUN-2002 (first entry)
DE Mouse novel neurotrophic factor NNT1.
XX
XX Mouse; NNT1; neurotrophic factor; IGF-related disease;
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.
OS Mus sp.
XX
XX WO200215977-A2.
PN 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US25906.
PF 18-AUG-2000; 2000US-226436P.
PR 16-AUG-2001; 2001US-0931704.
XX
XX (AMGE-) AMGEN INC.
PA
PI Senaldi G;
XX
XX WPI; 2002-280867/32.
DR N-PSDB; ABRK1649.
XX
XX
XX Treating Immunoglobulin E-related disease, modulating IGE levels in a
PT patient, preventing IGE-related disease and treating allergic diseases,
PT involves administering NNT-1 inhibitor to a patient -
XX
XX Claim 2; Fig 5; 63pp; English.
PS
XX
XX The invention relates to treating Immunoglobulin E (IGE)-related disease,
CC modulating IGE levels in a patient, preventing an IGE-related disease,
CC and treating allergic diseases, comprising administering a
CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
CC inhibitor to a patient. Also included are a method of diagnosing an
CC IGE-related disease or susceptibility to an IGE-related disease, by
CC determining the presence or amount of expression of an NNT1 polypeptide
CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
CC occurring variant, and diagnosing an IGE-related disease or
CC susceptibility of an IGE-related disease based on the presence or amount
CC of expression of the polypeptide and a pharmaceutical composition for use
CC in treating IGE-related disease, comprising the NNT1 inhibitor.
CC The NNT1 inhibitor is useful for preventing and treating IGE-related
CC disease, modulating IGE levels, and treating allergic diseases e.g.
CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,
CC pollinosis, asthma, immune diseases and disorders, diseases involving
CC abnormal cell proliferation including cancer, arteriosclerosis and

CC vascular restenosis, diseases and conditions relating to dysfunction of
CC immune system including rheumatoid arthritis, psoriatic arthritis,
CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,
CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
CC bowel disease, transplant rejection, and graft versus host disease, and
CC reproductive diseases and disorders including infertility, miscarriage,
CC preterm labour and delivery, and endometriosis. The present sequence
CC represents Mouse NNT1.
XX
SQ Sequence 225 AA:
Query Match 97.3%; Score 1193; DB 23; Length 225;
Best Local Similarity 96.9%; Pred. No. 4.3e-115;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDLRAGDSWGMIACTVLMHLPAPVAPALNRIGDPPGPSIQKTYDITRYLHQLSLAGT 60
DB 1 MDLRAGDSWGMIACTVLMHLPAPVAPALNRIGDPPGPSIQKTYDITRYLHQLSLAGT 60
QY 61 YNATGPPFNEPDPRLGAEITLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLRGL 120
DB 61 YNATGPPFNEPDPRLGAEITLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLRGL 120
QY 121 NROAATAEIRSLAHFCTSLQGLGSIAGVMAALGYPPLPGTEPTWTPGPAHSDFLQ 180
DB 121 NROAATAEIRSLAHFCTSLQGLGSIAGVMAALGYPPLPGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKELQTWLMRSKADFNRLKKKQOPPAATVTLHGAHGF 225
DB 181 KMDDFWLKELQTWLMRSKADFNRLKKKQOPPAATVTLHGAHGF 225

Search completed: February 9, 2004, 06:16:54
Job time : 37.5 secs

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OM protein - protein search, using ew model

Run on: February 9, 2004, 06:17:01 ; Search time 33 Seconds
(without alignments)
1427.606 Million cell updates/sec

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Perfect score: 1226
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1226	100.0	225	9	US-09-931-704-2
2	1226	100.0	225	15	US-10-212-793-2
3	1193	97.3	225	9	US-09-931-704-5
4	885	72.2	164	9	US-09-864-761-40014
5	124.5	10.2	203	15	US-10-212-793-3
6	118.5	9.7	203	10	US-09-896-856-3
7	118.5	9.7	203	12	US-10-407-303-3
8	118.5	9.7	203	15	US-10-107-931-3
9	96.5	7.9	243	9	US-09-810-052-5
10	96.5	7.9	243	11	US-09-791-497-8
11	96.5	7.9	243	14	US-10-000-776-6
12	92.5	7.5	860	15	US-10-156-761-11445
13	91.5	7.5	201	10	US-09-901-540-3
14	91.5	7.5	201	10	US-09-896-856-8
15	91.5	7.5	201	10	US-09-901-257-3

16	91.5	7.5	201	12	US-10-407-303-8	Sequence 8, Appl1
17	91.5	7.5	201	15	US-10-107-931-8	Sequence 8, Appl1
18	91.5	7.5	201	15	US-10-212-793-4	Sequence 4, Appl1
19	91.5	7.5	1182	15	US-10-024-368-6	Sequence 6, Appl1
20	91	7.4	195	10	US-09-770-361-5	Sequence 5, Appl1
21	91	7.4	195	12	US-10-281-643-5	Sequence 5, Appl1
22	91	7.4	195	12	US-10-383-916-5	Sequence 5, Appl1
23	91	7.4	195	15	US-10-226-759-5	Sequence 5, Appl1
24	91	7.4	242	11	US-09-791-497-2	Sequence 2, Appl1
25	91	7.4	242	14	US-10-000-776-2	Sequence 2, Appl1
26	90	7.3	232	9	US-09-810-052-2	Sequence 2, Appl1
27	88.5	7.2	1429	12	US-10-028-374-3	Sequence 3, Appl1
28	88.5	7.2	1429	12	US-10-183-770-3	Sequence 3, Appl1
29	87.5	7.1	1207	15	US-10-024-368-5	Sequence 5, Appl1
30	85	6.9	727	12	US-10-231-913-8	Sequence 8, Appl1
31	84.5	6.9	389	12	US-10-369-493-22941	Sequence 22941, A
32	84	6.9	411	12	US-10-369-493-562	Sequence 562, App
33	84	6.9	876	12	US-10-074-511-110	Sequence 110, App
34	83.5	6.8	275	15	US-10-156-761-12256	Sequence 12256, A
35	83	6.8	469	15	US-10-156-761-9695	Sequence 9695, Ap
36	83	6.8	625	10	US-09-771-161A-242	Sequence 242, App
37	83	6.8	625	10	US-09-771-161A-243	Sequence 243, App
38	82.5	6.7	984	15	US-10-024-368-2	Sequence 2, Appl1
39	82.5	6.7	1189	15	US-10-024-368-4	Sequence 4, Appl1
40	82.5	6.7	1189	15	US-10-122-013-17	Sequence 17, Appl1
41	82	6.7	200	10	US-09-770-361-8	Sequence 8, Appl1
42	82	6.7	200	12	US-10-281-643-8	Sequence 8, Appl1
43	82	6.7	200	12	US-10-383-916-8	Sequence 8, Appl1
44	82	6.7	200	15	US-10-226-759-8	Sequence 8, Appl1
45	81.5	6.6	218	10	US-09-893-737-28	Sequence 28, Appl1

ALIGNMENTS

RESULT 1
US-09-931-704-2
Sequence 2, Application US/09931704
Patent No. US30020041873A1
GENERAL INFORMATION:
APPLICANT: Senaldi, Giorgio
TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using
FILE REFERENCE: A-695
CURRENT APPLICATION NUMBER: US/09/931,704
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/226,436
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
US-09-931-704-2

Query Match	100.0%	Score 1226;	DB 9;	Length 225;
Best Local Similarity	100.0%	Prod. No. 5.9e-115;		
Matches 225;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0;
QY	1	MDLRAGDSWGMCLACTVLMHLPAVPAALNRKGDPPGPGSIQKTYDLYLEHQLSLAGT	60	
DB	1	MDLRAGDSWGMCLACTVLMHLPAVPAALNRKGDPPGPGSIQKTYDLYLEHQLSLAGT	60	
QY	61	YLYNYGPPENPDENPRPGAETLPRATVDLEVMRLNDKRLRTQNYEAYSHLCTYRGL	120	
DB	61	YLYNYGPPENPDENPRPGAETLPRATVDLEVMRLNDKRLRTQNYEAYSHLCTYRGL	120	
QY	121	NROATATLRSLAHFCTSLGGLGSLAGVMAALGYPLQPLPGTEPTWGPASDFLQ	180	
DB	121	NROATATLRSLAHFCTSLGGLGSLAGVMAALGYPLQPLPGTEPTWGPASDFLQ	180	
QY	181	KMDDEWLKELQYLMRSKQFNRLKKMGPPAAVTLHGANGF	225	

Db 181 KMDDFWLKEIQTWLMRSKADFNRLKKKQPPAAAVTLHLGAHGF 225

RESULT 2
US-10-212-793-2

Sequence 2, Application US/10212793
Publication No. US20030087395A1
GENERAL INFORMATION:
APPLICANT: Shi et al.
TITLE OF INVENTION: Cardiotrophin-Like Cytokine
FILE REFERENCE: PF385D1C1
CURRENT APPLICATION NUMBER: US/10/212,793
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 09/438,299
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/106,182
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: US 60/051,311
PRIOR FILING DATE: 1997-06-30
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 2
LENGTH: 225
TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: signal
LOCATION: (-27)..(-1)
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(198)
US-10-212-793-2

Query Match 100.0% Score 1226; DB 15; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.9e-115;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACICTVLMHLPAYPALNRTGDPGPGPSIOKTYDLTRYLEHQLSLQGT 60
Db 1 MDLRAGDSWGMACICTVLMHLPAYPALNRTGDPGPGPSIOKTYDLTRYLEHQLSLQGT 60
QY 61 YLNYLGPPNPEDFPNRLGAETLPRATVDEWVMSLNDKRLTONYEAYSHLCTYRGL 120
Db 61 YLNYLGPPNPEDFPNRLGAETLPRATVDEWVMSLNDKRLTONYEAYSHLCTYRGL 120
QY 121 NROATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPGLPTEPTWTPGPAHSDFLQ 180
Db 121 NROATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPGLPTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKEIQTWLMRSKADFNRLKKKQPPAAAVTLHLGAHGF 225
Db 181 KMDDFWLKEIQTWLMRSKADFNRLKKKQPPAAAVTLHLGAHGF 225

RESULT 3
US-09-931-704-5

Sequence 5, Application US/09931704
Patent No. US20020044873A1
GENERAL INFORMATION:
APPLICANT: Senaldi, Giorgio
TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using N
FILE REFERENCE: A-695
CURRENT APPLICATION NUMBER: US/09/931,704
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/226,436
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 225
TYPE: PRT
ORGANISM: Murine

US-09-931-704-5

Query Match 97.3% Score 1193; DB 9; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.2e-111;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACICTVLMHLPAYPALNRTGDPGPGPSIOKTYDLTRYLEHQLSLQGT 60
Db 1 MDLRAGDSWGMACICTVLMHLPAYPALNRTGDPGPGPSIOKTYDLTRYLEHQLSLQGT 60
QY 61 YLNYLGPPNPEDFPNRLGAETLPRATVDEWVMSLNDKRLTONYEAYSHLCTYRGL 120
Db 61 YLNYLGPPNPEDFPNRLGAETLPRATVDEWVMSLNDKRLTONYEAYSHLCTYRGL 120
QY 121 NROATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPGLPTEPTWTPGPAHSDFLQ 180
Db 121 NROATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPGLPTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKEIQTWLMRSKADFNRLKKKQPPAAAVTLHLGAHGF 225
Db 181 KMDDFWLKEIQTWLMRSKADFNRLKKKQPPAAAVTLHLGAHGF 225

RESULT 4
US-09-864-761-40014

Sequence 40014, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomic-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29

Db 141 AALGAARGPGEPTVATLFTANSTAGIFSAKVLGFHVCGHGEWVSRTEGDLGQL 197

RESULT 7

US-10-407-303-3

Sequence 3, Application US/10407303

Publication No. US20040006018A1

GENERAL INFORMATION:

APPLICANT: Baker, Joffre

APPLICANT: Chien, Kenneth

APPLICANT: King, Kathleen

APPLICANT: Pennica, Diane

APPLICANT: Wood, William

TITLE OF INVENTION: Methode of Stimulating the Proliferation and

TITLE OF INVENTION: Differentiation of Satellite Cells Into Myoblasts by

TITLE OF INVENTION: Contact with CT-1

FILE REFERENCE: P0994R1D2C1

CURRENT APPLICATION NUMBER: US/10/407,303

CURRENT FILING DATE: 2003-04-03

PRIOR APPLICATION NUMBER: US 09/724,772

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: US 08/797,014

PRIOR FILING DATE: 1997-02-07

PRIOR APPLICATION NUMBER: US 60/049,998

PRIOR FILING DATE: 1996-02-14

NUMBER OF SEQ ID NOS: 8

SEQ ID NO: 3

LENGTH: 203

TYPE: PRT

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: Amino Acid

LOCATION: Full

OTHER INFORMATION:

US-10-407-303-3

Query Match

Best Local Similarity 9.7%; Score 118.5; DB 12; Length 203;

Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

Db 40 IOKTYDLTRYEHQRLSLAGTYLNTLGPPEPDPNPRL--GATLPRTATVLEWRS 96

Db 27 IROTHNLARLTLTKYAEQLEBYVOQGEPFGLPGFSPRLPLAGLSGAPSHAGLPV-- 83

Qy 97 LNDKRLTQNYEAVSHLLCYLRGLNRQA-----TAEIRSLAHCTSLQGLGSIAGVM 151

Db 84 ---SERLRQDAALSVLPALIDAVRRQAEINPRAPIRLRSLEDAARQVRALGAAVEVTL 140

Qy 152 AALGYPL--POPPLGTEPT--WTPGPAHSDFLQKMDFWLKLKELQTLWMSAKDPNRL 205

Db 141 AALGAARGPGEPTVATLFTANSTAGIFSAKVLGFHVCGHGEWVSRTEGDLGQL 197

RESULT 8

US-10-107-931-3

Sequence 3, Application US/10107931

Publication No. US20030054550A1

GENERAL INFORMATION:

APPLICANT: Baker, Joffre

APPLICANT: Chien, Kenneth

APPLICANT: King, Kathleen

APPLICANT: Pennica, Diane

APPLICANT: Wood, William

TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/107,931

FILING DATE: 26-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/364,187

FILING DATE: 30-Jul-1999

APPLICATION NUMBER: 08/286,304

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: 894P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1896

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 203 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-107-931-3

Query Match

Best Local Similarity 9.7%; Score 118.5; DB 15; Length 203;

Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

Qy 40 IOKTYDLTRYEHQRLSLAGTYLNTLGPPEPDPNPRL--GATLPRTATVLEWRS 96

Db 27 IROTHNLARLTLTKYAEQLEBYVOQGEPFGLPGFSPRLPLAGLSGAPSHAGLPV-- 83

Qy 97 LNDKRLTQNYEAVSHLLCYLRGLNRQA-----TAEIRSLAHCTSLQGLGSIAGVM 151

Db 84 ---SERLRQDAALSVLPALIDAVRRQAEINPRAPIRLRSLEDAARQVRALGAAVEVTL 140

Qy 152 AALGYPL--POPPLGTEPT--WTPGPAHSDFLQKMDFWLKLKELQTLWMSAKDPNRL 205

Db 141 AALGAARGPGEPTVATLFTANSTAGIFSAKVLGFHVCGHGEWVSRTEGDLGQL 197

RESULT 9

US-09-810-052-5

Sequence 5, Application US/09810052

Patent No. US20020009775A1

GENERAL INFORMATION:

APPLICANT: Conklin, Darrell C.

APPLICANT: Presnell, Scott R.

TITLE OF INVENTION: HELICAL PROTEIN ZALPHA51

FILE REFERENCE: 00-24

CURRENT APPLICATION NUMBER: US/09/810,052

CURRENT FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/190,410

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/199,443

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PastsEQ for Windows Version 3.0

SEQ ID NO: 5

LENGTH: 243

TYPE: PRT

ORGANISM: Homo sapiens

US-09-810-052-5

Query Match

Best Local Similarity 7.9%; Score 96.5; DB 9; Length 243;

Matches 58; Conservative 26; Mismatches 104; Indels 57; Gaps 9;

[illegible]

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RESULT 10
US-09-791-497-B
; Sequence 8, Application US/09791497
; Publication No. US20030008343A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kaeteleijn, Robert A.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Pfanz, Stefan
; TITLE OR INVENTION: Mammalian Cytokines; Related Reagents
; FILE REFERENCE: D01040X2
; CURRENT APPLICATION NUMBER: US/09/791,497
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 243
; TYPE: PRT
; ORGANISM: primate; surmised Homo sapiens
US-09-791-497-B

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Query Match	7.9%	Score 96.5	DB 11	Length 243
Best Local Similarity	23.7%	Pred. NO. 0.21		
Matches	58	Conservative	104	Indels 57
				Gaps 9

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QY 47 TRYLEHQLRSLAGTYLN-----YLGRPFEPDPENPRRGAETLPRAATYDLEWMSLN 98
Db 54 ARKLSEVRQOARFASHLPGVNLILP-----LG-EGLPVSTTTPQAMRRLS 101
QY 99 DKURLTQNYEAYSHLCLYGLNROAAATLERR-SLAHCTSLGGLSGISNGWAALGYR 157
Db 102 DPEELCFISTTLQPFHAPLGGLGCTQGRWNTMERQLMAMRLDLRLDQHLRFQVYLAAGFN 161
QY 158 LPPD-----LPGNPPTWTPGPHASDPLQMDKDFWLLKELQWLIRMSAKDF 202
Db 162 LPPEEEEEEEEEBERKGLIPGALGALQSPQVSPQLSTYRLLHSLLEVLISRAVEL 221

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RESULT 11
US-10-000-776-6
Sequence 6, Application US/10000776
Publication No. US20020164609A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Pfanz, Stéfan, K.-H.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, Jose F.
APPLICANT: Remick, Donna
APPLICANT: de Waal Malefyt, Rene
APPLICANT: Cheung, Jeanne
TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
FILE REFERENCE: DX0104093
CURRENT APPLICATION NUMBER: US/10/000,776
PRIORITY FILING DATE: 2001-11-30
PRIORITY APPLICATION NUMBER: 09/791,497
PRIORITY FILING DATE: 2001-02-22
PRIORITY APPLICATION NUMBER: 09/627,897
PRIORITY FILING DATE: 2000-07-27
PRIORITY APPLICATION NUMBER: 60/146,581
PRIORITY FILING DATE: 1999-07-30
PRIORITY APPLICATION NUMBER: 60/147,763
PRIORITY FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-776-6

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Query Match	7.9%	Score 96.5	DB 14	Length 243
Best Local Similarity	23.7%	Pred. No. 0.21		
Matches 58	Conservative 26	Mismatches 104	Indels 57	Gaps 9

QY 4 TRYLEHQLSLAGTYLN-----YLDPFRPEPDPFNPRRGAETLRPATYDLVMSLN 98
Db 54 ARKLISLVKQAHRRFAESHLPQVNL YLTP-----LG-EQLPVS LTFQAMRRLS 101
QY 99 DKRLTQNTVEAYSHLLCYLRGLNROATAELRR-SLAHFTSLQGLGSIAGVAAALGYP 151
Db 102 DPERLQFISTYLLQPRHAPLGSLGTGKRTNNERMQLMMRLDLNDRHLRFYLLAAGFN 161
QY 158 LPQP-----LPGETPTWTPGPAHSDFLQKMDFWLLKELQTLWRSAKDP 203
Db 162 LPPEEEEEEEEEERKGLLPALGSLAGPAQVSPQLLSTYRLHLSLELVLSRAVREL 221
QY 203 NRLKK 207
Db 222 LLLSK 226

RESULT 12
US-10-156-761-11445
Sequence 11445, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, YOSHIO
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156, 761/
CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 11445
 ; LENGTH: 860
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 US-10-156-761-11445

Query Match 7.5%; Score 92.5; DB 15; Length 860;
 Best Local Similarity 27.2%; Pred. No. 2.7;
 Matches 56; Conservative 22; Mismatches 101; Indels 27; Gaps 9;

QY 5 AGDSMGLACLCVLA--WLPVAPVLRNRGDPG-----PGSICKYDITRY 49
 DB 288 AQAATTAATVBEELKDMH--EGGPAVLRAGLSVRDCKRTAVALDVPEPTAAPWELT-Y 345
 QY 50 LEHOLSLAGTYLNYLGPFPNEPDENPPRLGAETLPRAVDLEVRSLNDKRLTONVEA 109
 DB 346 AAGLASDGEABERYAATPAYDEWLELP--AAERMSRLAT---AWLAATRTAGVIGGRNA 400
 QY 110 YSHLCYL-RGLNRQATLRLSLAHFCTSLQGLGSIAGVMAALGYPLPQPLDPTPT 168
 DB 401 KERTLSALGPGLDRSAASEVRRLVALLADLPEGASAPASVIALRLW--ERPLRGTHPS 458
 QY 169 WTP--GPAHSDFLQKMDDFWLKELQ 192
 DB 459 PSPSSAPSSDDLKTRRLAEWTLSAE 484

RESULT 13

US-09-901-540-3
 ; Sequence 3, Application US/09901540
 ; Patent No. US20020102622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Botstein, David
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Lawrence, David A.
 ; APPLICANT: Pennica, Diane
 ; APPLICANT: Roy, Margaret A.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Cardiotrophin-1 Compositions and Methods for the
 ; FILE REFERENCE: P2533D2
 ; CURRENT APPLICATION NUMBER: US/09/901,540
 ; CURRENT FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: 09/648,258
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: US 09/033,114
 ; PRIOR FILING DATE: 1998-03-02
 ; PRIOR APPLICATION NUMBER: US 08/733,850
 ; PRIOR FILING DATE: 1996-10-18
 ; PRIOR APPLICATION NUMBER: US 08/443,129
 ; PRIOR FILING DATE: 1995-05-17
 ; PRIOR APPLICATION NUMBER: US 08/286,304
 ; PRIOR FILING DATE: 1994-08-05
 ; PRIOR APPLICATION NUMBER: US 08/233,609
 ; PRIOR FILING DATE: 1994-04-25
 ; PRIOR APPLICATION NUMBER: US 60/113,296
 ; PRIOR FILING DATE: 1998-12-22
 ; NUMBER OF SEQ ID NOS: 6
 ; SEQ ID NO 3
 ; LENGTH: 201
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-901-540-3

Query Match 7.5%; Score 91.5; DB 10; Length 201;
 Best Local Similarity 25.9%; Pred. No. 0.51;
 Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;

QY 40 IQKTYDLTRYLEHQRLSLAGTYLNYLGPFPNEPDENPPRLGAETLPRAVDLEVRSLND 99
 DB 27 IQRTSLAHLLTKVAEQLOEVYQGDPPGILPSPSPRLPVAGL-SAPAPSHAGLPHE 85
 QY 100 KRLTONTEAYSHLCYLRGLNRQAA-----TAEIRSLAHFCTSLQGLGSIAGVMAAL 154
 DB 86 RLRL--DAAALAALEPPLLDVACRQAEINPPAPRLRLRLIEDAARQARALGAAVEALLAAL 143
 QY 155 GYPLPQPLDPTPT---TWTGPAHSDFLQKMDDFWLKELQTWLMSAKDFNRL 205
 DB 144 G--AANRGPRAEPAPATASASATGVPAKVGLRVCGLYRWLSRTGDLGQL 195

RESULT 14

US-09-896-856-8
 ; Sequence 8, Application US/09896856
 ; Patent No. US20020137189A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Joffre
 ; APPLICANT: Chien, Kenneth
 ; APPLICANT: King, Kathleen
 ; APPLICANT: Pennica, Diane
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Winpatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/896,856
 ; FILING DATE: 29-Jun-2001
 ; CLASSIFICATION: <unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/733,850
 ; FILING DATE: 18-OCT-1996
 ; APPLICATION NUMBER: US 08/471,112
 ; FILING DATE: 06-JUN-1995
 ; APPLICATION NUMBER: 08/233,609
 ; FILING DATE: 25-APR-1994
 ; APPLICATION NUMBER: 08/286304
 ; FILING DATE: 05-AUG-1994
 ; APPLICATION NUMBER: 08/443129
 ; FILING DATE: 17-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conley, Delindre L.
 ; REGISTRATION NUMBER: 36,487
 ; REFERENCE/DOCKET NUMBER: P0894P1D2C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-2066
 ; TELEFAX: 415/952-9881
 ; TELEEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 201 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-896-856-8

Query Match 7.5%; Score 91.5; DB 10; Length 201;
 Best Local Similarity 25.9%; Pred. No. 0.51;
 Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;
 QY 40 IQKTYDLTRYLEHQRLSLAGTYLNYLGPFPNEPDENPPRLGAETLPRAVDLEVRSLND 99

Db 27 IROTHSLAHLTRKYAEQLQEVYQLOGDFGLPSFSPRLPVAGL-SAPAPSHAGLPVHE 85
QY 100 KURLTONYEAYSHLCTYLGRLNROA-----TALRSLAHFCTSLQGLIGSIAGYMAAL 154
Db 86 RLRL--DAAALALPPLDAVCRQAELNPRAPRLRLLEDARQAARALGAAVEALLAAL 143
QY 155 GYPLPQLPCTEP---TWTPGPAHSDPLQMDPFMLKELOTWLRSAKDFNRL 205
Db 144 G--AANRGPAEPAPATASASATGVFPAKVGLGRVCGLYREWLSRTEGDLGQL 195

RESULT 15

US-09-901-257-3
Sequence 3, Application US/09901257
Patent No. US20020146707A1.
GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Lawrence, David A.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret A.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Cardiotrophin-1 Compositions and Methods for the
FILE REFERENCE: P2533D3
CURRENT APPLICATION NUMBER: US/09/901,257
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/548,252
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 09/033,114
PRIOR FILING DATE: 1998-03-02
PRIOR APPLICATION NUMBER: US 08/733,850
PRIOR FILING DATE: 1996-10-18
PRIOR APPLICATION NUMBER: US 08/443,129
PRIOR FILING DATE: 1995-05-17
PRIOR APPLICATION NUMBER: US 08/286,304
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: US 08/233,609
PRIOR FILING DATE: 1994-04-25
PRIOR APPLICATION NUMBER: US 60/113,296
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
LENGTH: 201
TYPE: PRT
ORGANISM: Human
US-09-901-257-3

Query Match 7.5%; Score 91.5; DB 10; Length 201;
Best Local Similarity 25.9%; Pred. No. 0.51; Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;
QY 40 IOKTYDLTRYELBQLSLAGTYLVYLGPPNEBDFNPRPGAETLPRATVDLEWMSLND 99
Db 27 IROTHSLAHLTRKYAEQLQEVYQLOGDFGLPSFSPRLPVAGL-SAPAPSHAGLPVHE 85
QY 100 KURLTONYEAYSHLCTYLGRLNROA-----TALRSLAHFCTSLQGLIGSIAGYMAAL 154
Db 86 RLRL--DAAALALPPLDAVCRQAELNPRAPRLRLLEDARQAARALGAAVEALLAAL 143
QY 155 GYPLPQLPCTEP---TWTPGPAHSDPLQMDPFMLKELOTWLRSAKDFNRL 205
Db 144 G--AANRGPAEPAPATASASATGVFPAKVGLGRVCGLYREWLSRTEGDLGQL 195

Search completed: February 9, 2004, 06:26:16
Job time : 34 secs

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OM protein - protein search, using SW model

Run on: February 9, 2004, 06:15:41; Search time 15 Seconds

(without alignments)
634.663 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226

Sequence: 1 MDLRAGDSWGMALCLCTVLM.....KKKQPPAAAVTLHGAGHF 225

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1226	100.0	225	1	US-08-792-019B-2
2	1226	100.0	225	2	US-09-106-182-2
3	1226	100.0	225	3	US-08-988-819-2
4	1226	100.0	225	3	US-09-016-534-2
5	1193	97.3	225	1	US-08-792-019B-5
6	1193	97.3	225	3	US-08-988-819-5
7	1193	97.3	225	3	US-09-016-534-5
8	124.5	10.2	203	3	US-09-106-182-3
9	118.5	9.7	203	1	US-08-233-609-3
10	118.5	9.7	203	1	US-08-444-083-3
11	118.5	9.7	203	1	US-08-286-304-3
12	118.5	9.7	203	1	US-08-442-745-3
13	118.5	9.7	203	1	US-08-443-129-3
14	118.5	9.7	203	1	US-08-443-952-3
15	118.5	9.7	203	1	US-08-443-130-3
16	118.5	9.7	203	3	US-08-898-911-3
17	118.5	9.7	203	5	PCT-US95-04467-3
18	91.5	7.5	201	1	US-08-444-083-8
19	91.5	7.5	201	1	US-08-286-304-8
20	91.5	7.5	201	1	US-08-442-745-8
21	91.5	7.5	201	1	US-08-443-129-8
22	91.5	7.5	201	1	US-08-443-952-8
23	91.5	7.5	201	1	US-08-443-130-8
24	91.5	7.5	201	1	US-08-443-130-8
25	91.5	7.5	201	3	US-08-792-019B-11
26	91.5	7.5	201	3	US-09-106-182-4
27	91.5	7.5	201	3	US-08-988-819-11
					Sequence 8, App1

28	91.5	7.5	201	3	US-09-016-534-11	Sequence 11, App1
29	91.5	7.5	201	4	US-09-648-183-3	Sequence 3, App1
30	91.5	7.5	201	5	PCT-US95-04467-8	Sequence 6, App1
31	91.5	7.5	1182	4	US-09-287-354-6	Sequence 5, App1
32	91	7.4	195	1	US-07-959-284-5	Sequence 5, App1
33	91	7.4	195	2	US-08-308-736A-5	Sequence 5, App1
34	91	7.4	195	4	US-08-645-107A-5	Sequence 5, App1
35	91	7.4	195	4	US-09-197-349-5	Sequence 5, App1
36	91	7.4	195	4	US-09-031-693-5	Sequence 5, App1
37	91	7.4	195	5	PCT-US92-08258-2	Sequence 2, App1
38	91	7.4	195	5	PCT-US93-09649A-5	Sequence 2, App1
39	91	7.4	195	5	PCT-US93-09649-5	Sequence 5, App1
40	89	7.3	737	4	US-09-252-991A-22539	Sequence 22539, A
41	87.5	7.1	1207	2	US-09-287-354-5	Sequence 5, App1
42	85.5	7.0	560	2	US-08-756-317-11	Sequence 11, App1
43	84.5	6.9	426	4	US-09-252-991A-29288	Sequence 29288, A
44	84	6.9	200	3	US-08-949-155-4	Sequence 4, App1
45	84	6.9	200	4	US-09-819-964-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-08-792-019B-2
Sequence 2, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-019B-2
Query Match
Best Local Similarity 100.0%; Score 1226; DB 1; Length 225;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLRAGDSWGMALCLCTVLMHLPVAVPALNRTDPPGSPISIOKTYDLTRYLHQSLAGT 60
1 MDLRAGDSWGMALCLCTVLMHLPVAVPALNRTDPPGSPISIOKTYDLTRYLHQSLAGT 60
QY 61 YNNTGPPPNEDNPPRLGATTLPRATYDLEVMASLNDKRLTLTONYEVSHLCTYKGL 120
61 YNNTGPPPNEDNPPRLGATTLPRATYDLEVMASLNDKRLTLTONYEVSHLCTYKGL 120
DB 61 YNNTGPPPNEDNPPRLGATTLPRATYDLEVMASLNDKRLTLTONYEVSHLCTYKRL 120
61 YNNTGPPPNEDNPPRLGATTLPRATYDLEVMASLNDKRLTLTONYEVSHLCTYKRL 120
QY 121 NQAAVTAELRRSLAFTCSLQGLSIGVMAALGYPLQPLRGTEPTTPGPAHSDFIQ 180
121 NQAAVTAELRRSLAFTCSLQGLSIGVMAALGYPLQPLRGTEPTTPGPAHSDFIQ 180

Db 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPOPLPGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225
Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225

RESULT 2

US-09-106-182-2
Sequence 2, Application US/09106182
Patent No. 6046035
GENERAL INFORMATION:
APPLICANT: Shi, Yangu
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Cardiotrophin-Like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF385
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-182-2

Query Match 100.0%; Score 1226; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-129; Indels 0; Gaps 0;
Matches 225; Conservative 0; Mismatches 0;

QY 1 MDLRAGDSWGMACICTVLMHLPAVPALNRTGDPGPGPSIOKTYDLYLREHQLSLAGT 60
Db 1 MDLRAGDSWGMACICTVLMHLPAVPALNRTGDPGPGPSIOKTYDLYLREHQLSLAGT 60
QY 61 YLNYLGPPNPEDFPNPRIGAETLPRAVVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
Db 61 YLNYLGPPNPEDFPNPRIGAETLPRAVVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
QY 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPOPLPGTEPTWTPGPAHSDFLQ 180
Db 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPOPLPGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225
Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225

RESULT 3

US-08-988-819-2

Sequence 2, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-988-819-2

Query Match 100.0%; Score 1226; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-129; Indels 0; Gaps 0;
Matches 225; Conservative 0; Mismatches 0;

QY 1 MDLRAGDSWGMACICTVLMHLPAVPALNRTGDPGPGPSIOKTYDLYLREHQLSLAGT 60
Db 1 MDLRAGDSWGMACICTVLMHLPAVPALNRTGDPGPGPSIOKTYDLYLREHQLSLAGT 60
QY 61 YLNYLGPPNPEDFPNPRIGAETLPRAVVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
Db 61 YLNYLGPPNPEDFPNPRIGAETLPRAVVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
QY 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPOPLPGTEPTWTPGPAHSDFLQ 180
Db 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPOPLPGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225
Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225

RESULT 4

US-09-016-534-2
Sequence 2, Application US/09016534
Patent No. 6143874
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: ELIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS

STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-09-016-534-2

Query Match 100.0%; Score 1226; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 2,2e-129;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVLMHLPVAVPALNRRTGDPGPGPSIQKTYDLTRYLEHQLRSAGT 60
DB 1 MDLRAGDSWGMCLACTVLMHLPVAVPALNRRTGDPGPGPSIQKTYDLTRYLEHQLRSAGT 60
QY 61 YLNYLGPPNEPDPNPRLGAETLPRAVVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPNEPDPNPRLGAETLPRAVVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
QY 121 NRQAATAEIARRSLAHCSTSLQGLSIAGVMAALGYPLPOLPGTEPTWTPGPAHSDFLQ 180
DB 121 NRQAATAEIARRSLAHCSTSLQGLSIAGVMAALGYPLPOLPGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPPAAVTTLHGAGHF 225
DB 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPPAAVTTLHGAGHF 225

RESULT 5
US-08-792-019B-5
Sequence 5, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-019B-5

Query Match 97.3%; Score 1193; DB 1; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.1e-125;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVLMHLPVAVPALNRRTGDPGPGPSIQKTYDLTRYLEHQLRSAGT 60
DB 1 MDLRAGDSWGMCLACTVLMHLPVAVPALNRRTGDPGPGPSIQKTYDLTRYLEHQLRSAGT 60
QY 61 YLNYLGPPNEPDPNPRLGAETLPRAVVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPNEPDPNPRLGAETLPRAVVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
QY 121 NRQAATAEIARRSLAHCSTSLQGLSIAGVMAALGYPLPOLPGTEPTWTPGPAHSDFLQ 180
DB 121 NRQAATAEIARRSLAHCSTSLQGLSIAGVMAALGYPLPOLPGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPPAAVTTLHGAGHF 225
DB 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPPAAVTTLHGAGHF 225

RESULT 6
US-08-988-819-5
Sequence 5, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-988-819-5
Query Match 97.3%; Score 1193; DB 3; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.1e-125;

Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACCTVLMHLPAVPALNRGTDPGGPSIQKTYDLTRYLHQLSLAGT 60
DB 1 MDLRAGDSWGMACCTVLMHLPAVPALNRGTDPGGPSIQKTYDLTRYLHQLSLAGT 60

QY 61 YLNYIGPPNEPDNPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYIGPPNEPDNPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120

QY 121 NQOATAEIRSLAHFCTSLQGLSIGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180
DB 121 NQOATAEIRSLAHFCTSLQGLSIGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180

QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPPAATVTLHGAHGF 225
DB 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPPAATVTLHGAHGF 225

RESULT 7

US-09-016-534-5
; Sequence 5, Application US/09016534

; Patent No. 6143974
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-534-5

Query Match 97.3%; Score 1193; DB 3; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.1e-125;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACCTVLMHLPAVPALNRGTDPGGPSIQKTYDLTRYLHQLSLAGT 60
DB 1 MDLRAGDSWGMACCTVLMHLPAVPALNRGTDPGGPSIQKTYDLTRYLHQLSLAGT 60

QY 61 YLNYIGPPNEPDNPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYIGPPNEPDNPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120

QY 121 NQOATAEIRSLAHFCTSLQGLSIGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180
DB 121 NQOATAEIRSLAHFCTSLQGLSIGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180

QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPPAATVTLHGAHGF 225
DB 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPPAATVTLHGAHGF 225

RESULT 8

US-09-106-182-3
; Sequence 3, Application US/09106182

; Patent No. 6046035
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,182
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/051,053
; FILING DATE: 30-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF385
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-106-182-3

Query Match 10.2%; Score 124.5; DB 3; Length 203;
Best Local Similarity 28.1%; Pred. No. 6.7e-06;
Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;

QY 40 IQKTYDLTRYLHQLSLAGTYLNYLGPNEPDNPRL---GAETLPRATVDLEWRS 96
DB 27 IROTINLARLTLKYADQLLEBYVOOGEPFGLPGPSPPRLLAGISGPAHAGLPV--- 83

QY 97 LNDKRLTONYEAYSHLLCYLRGINROA-----TAELRSLAHFCTSLQGLSIGVMA 151
DB 84 ---SERLRQDAALASALPALIDAVRRQAEINPPARLRLSLDPAARQVRLGAHVETVL 140

QY 152 AALGY----PLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLKELQTLWLRSAKDFNRL 205
DB 141 AALGAAGVPEPEV-AISALFTGNSAAGVSAVYLGLHVGGLGGEWVSRTEGDLGQL 197

RESULT 9

US-08-233-609-3
; Sequence 3, Application US/08233609

MEDIUM TYPE: 5.25 inch,360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genemtech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,304
 FILING DATE: 05-AUG-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/233609
 FILING DATE: 25-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,616
 REFERENCE/DOCKET NUMBER: 894P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1896
 TELEFAX: 415/952-9881
 TELEEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 203 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-286-304-3

Query Match	9.7%;	Score 118.5;	DB 1;	Length 203;
Best Local Similarity	28.8%;	Pred. No. 3.1e-05;		
Matches	51;	Conservative	21;	Mismatches 88;
			Indels	17;
			Gaps	5

[illegible]

RESULT 12
 US-08-442-745-3
 Sequence 3, Application US/08442745
 Patent No. 5624806
 GENERAL INFORMATION:
 APPLICANT: Baker, Joffe
 APPLICANT: Chien, Kenneth
 APPLICANT: King, Kathleen
 APPLICANT: Pennica, Diane
 APPLICANT: Wood, William
 TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/442,745
 FILING DATE: 17-may-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/333609

1 FILING DATE: 25-APR-1994
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 08/286304
4 FILING DATE: 05-AUG-1994
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Torchia, Timothy E.
7 REGISTRATION NUMBER: 56,700
8 REFERENCE/DOCKET INFORMATION: 894P1D1D1
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: 415/225-8674
11 TELEFAX: 415/952-9881
12 TELEEX: 910/371-7168
13 INFORMATION FOR SEQ. ID NO: 3:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 203 amino acids
16 TYPE: amino acid
17 TOPOLOGY: linear
18
19 US-08-442-745-3

Query Match	9.7%;	Score 118.5;	DB 1;	Length 203;
Best Local Similarity	28.8%;	Pred. No. 3.1e-05;		
Matches	51;	Conservative	21;	Mismatches 88;
				Indels 17;
				Gaps 5.

```

QY      40  ICKYVLTLYEHLQRLSLAGTYANTGSPFNPBPDPNPRL---GAETLLPRATYVULEYWR 96
      27  IRTNHLIAELLTKRYAQBLEEVVQOQGFGLGFPSPPRPLMALGSPAPSHGLPV--- 83
QY      97  LNDKLTNTONYEASHLLCYLRGLNROA-----TAEIRSLAFCTSLQGLGSGINVM 151
      84  ---SERLRDAAALSTVLPALDAVRRRAELNPRAPRLRSLIEDAPAOVRLGAAYETVL 140
QY      152  AALGYPL---POLPGTEPT-WTPGPAHSDPLQKMDFFWLKLELTQWLMRSAKDNPRLL 205
      141  AALGAAGAARGPEPVTVATLFTANSTAGIESAKVGVGVGCGLYGEWWSKTBGDDGQL 197

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RESULT 13
US-08-443-129-3
: Sequence 3, Application US/08443129
: Patent No. 5627073
: GENERAL INFORMATION:
: APPLICANT: Baker, Joffre
: APPLICANT: Chien, Kenneth
: APPLICANT: King, Kathleen
: APPLICANT: Pennica, Diane
: APPLICANT: Wood, William
: TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/443,129
: FILING DATE: 17-MAY-1995
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/233609
: FILING DATE: 25-APR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/286
: FILING DATE: 05-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 304
: FILING DATE: (null)

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ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-443-129-3

Query Match	9.7%	Score 118.5	DB 1	Length 203
Best Local Similarity	28.8%	Pred. No. 3.1e-05		
Matches	51	Conservative	21	Mismatches 88
			Indels	17
			Gaps	5

[illegible]

RESULT 14
US-08-443-952-3
Sequence 3, Application US/08443952
Patent No. 5679545
GENERAL INFORMATION:
APPLICANT: Baker, JoJoffe
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,952
FILING DATE: 17-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/213609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894P1D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881

```

; TELX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3
; SEQUENCE CHARACTERISTICS
; LENGTH: 203 amino acids.
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-443-952-3

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Query Match	9.7%	Score 118.5;	DB 1;	Length 203;
Best Local Similarity	38.8%	Prod No 3 10-05;		

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OY  40  OKYTYDRLRYVYEHQRLSLAGTYLNLGPPFNPDPNPRL----GAEYLPRAVYDLEWRS  96
Db  27  IRQTHNLRLRLTKCAEQBLEEYVQOGKBPGLGPGFSPPLPLAGSGAPASHAGLPV---  83
OY  97  LNDKLRLTQNTYEAASHLLCYLRGLNRQA-----TAIRLSRAHFCTSLQGLGSIAGYM  151
Db  84  ---SERLRQDAALASVLPALLDVARRRQAEINPPRPRLLRSLEDARQVRLGAAVETVL  140
OY  152  AALGYPL--PQPLPTEPT--WTPGFASDPLQKMDFMWLKELQTMRLMSAKDPNRL  205
Db  141  AALGAARAGPQPEPTVATLTFTANSTAGI FSAKVUGFHVCGLYGKGVNSTTEGDLGL  197

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1      RESULT 15
2      US-08-443-130-3
3      ; Sequence 3, Application US/08443130
4      ; Patent No. 5723585
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Baker, Joffre
7      ; APPLICANT: Chien, Kenneth
8      ; APPLICANT: King, Kathleen
9      ; APPLICANT: Pennica, Diane
10     ; APPLICANT: Wood, William
11     ; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses
12     ; TITLE OF INVENTION: Therefor
13     ; NUMBER OF SEQUENCES: 8
14     ; CORRESPONDENCE ADDRESS:
15     ; ADDRESSEE: Genentech, Inc.
16     ; STREET: 460 Point San Bruno Blvd
17     ; CITY: South San Francisco
18     ; STATE: California
19     ; COUNTRY: USA
20     ; ZIP: 94080
21     ; COMPUTER READABLE FORM:
22     ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
23     ; COMPUTER: IBM PC compatible
24     ; OPERATING SYSTEM: PC-DOS/MS-DOS
25     ; SOFTWARE: patin (Genentech)
26     ; CURRENT APPLICATION DATA:
27     ; APPLICATION NUMBER: US/08/443,130
28     ; FILING DATE: 17-MAY-1995
29     ; CLASSIFICATION: 435
30     ; PRIOR APPLICATION DATA:
31     ; APPLICATION NUMBER: 08/233609
32     ; FILING DATE: 25-APR-1994
33     ; PRIOR APPLICATION DATA:
34     ; APPLICATION NUMBER: 08/286304
35     ; FILING DATE: 05-AUG-1994
36     ; ATTORNEY/AGENT INFORMATION:
37     ; NAME: Torchia, Timothy E.
38     ; REGISTRATION NUMBER: 36,700
39     ; REFERENCE/DOCKET NUMBER: 894P1D3
40     ; TELECOMMUNICATION INFORMATION:
41     ; TELEPHONE: 415/225-8674
42     ; TELEFAX: 415/952-9881
43     ; TELETYPE: 910/371-7168
44     ; INFORMATION FOR SEQ ID NO: 3:
45     ; SEQUENCE CHARACTERISTICS:
46     ; LENGTH: 203 amino acids
47     ; TYPE: amino acid
48     ; TOPOLOGY: linear

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US-08-443-130-3

Query Match 9.7%; Score 118.5; DB 1; Length 203;
 Best Local Similarity 28.8%; Pred. No. 3.1e-05;
 Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

Qy	40	IQKTYDLTRYLEHQLRSLAGTYINYLGPPEPNEPDPRL--GAETLPRAIVDEWRS	96
Db	27	IRQTHNLRILITKYARQLLEEVYQQQGEPPGLPGFSPRLPLAGLSGPAPSHAGLPV---	83
Qy	97	LNDKRLTONYEAYSHLCTYLRGLNROA-----TAEFRSLAHFCTSLQGLGSIAGYM	151
Db	84	---SERLRQDPAALSVLPALLDAVRRQABLNPRAPLRLSLSDAARQVRAALGAAVETVL	140
Qy	152	AALGYPL--POLPGTEPT-WTPGPAHSDFLQMDDFMLIKEIQTWLWRSAXDFNRL	205
Db	141	AALGAARGPGEPEVTATLFTANSTAGIFSAKVLGFHVCGLYGEWVSRTBGDLGQL	197

Search completed: February 9, 2004, 06:25:00
 Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2004, 06:14:57 / Search time 10.5 Seconds

(without alignments)
1007.715 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226

Sequence: 1 MDLRAGDSWMLACTLVLM.....KKKQPPAAAVTLHGAGHF 225

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124.5	10.2	203	CTP1_RAT	063086 ratu
2	118.5	9.7	203	CTP1_MOUSE	060753 mus
3	94	7.7	423	CST_MOUSE	093he4 m
4	93	7.6	619	NXFL_HUMAN	09ub9 hom
5	91.5	7.5	201	CTP1_HUMAN	01619 hom
6	91.5	7.5	1182	HAIR_MOUSE	06145 mus
7	91	7.4	195	CNTF_CHICK	002011 gal
8	89.5	7.3	1313	MIP1_SCHPO	002011 gal
9	87.5	7.1	1181	HAIR_RAT	097609 ratu
10	86	7.0	1009	M2B2_HUMAN	09725 hom
11	85.5	7.0	560	PHAC_PSEOL	026596 pseu
12	84	6.9	200	CNTF_PIG	002732 sus
13	83	6.8	452	TLR_DROME	018102 dros
14	82.5	6.7	1189	HAIR_HUMAN	043593 dros
15	82	6.7	724	P85B_BOVIN	023726 bos
16	81	6.6	291	YM32_MYCTU	010515 myco
17	81	6.6	618	NXFL_RAT	088984 ratu
18	80.5	6.6	294	HUPR_RHOCA	037097 rho
19	80.5	6.6	870	BCA1_HUMAN	056645 hom
20	80.5	6.6	1473	NAL1_HUMAN	092000 hom
21	80	6.5	200	CNTF_RAT	020294 ratu
22	80	6.5	422	Y140_HUMAN	014153 hom
23	80	6.5	2261	RRLP_MUMPM	030929 mump
24	79	6.4	552	MPF2_MOUSE	09wv34 mus
25	79	6.4	1621	ALK_MOUSE	097793 mus
26	78.5	6.4	390	YL28_STRCO	040181 stre
27	78.5	6.4	1102	CARB_STRCO	09kxre stre
28	78	6.4	3680	DMD_CANPA	095922 canis
29	77	6.3	586	UL64_HCMVA	016727 huma
30	77	6.3	587	UL64_HCMVT	029639 huma
31	76.5	6.2	571	ATKA_MYCTU	096371 myco
32	76.5	6.2	572	SYM_AERPE	099cy3 aery
33	76.5	6.2	995	M2B2_PIG	028949 sus

34	76	6.2	296	RECO_ANASP	08yp19 anaba
35	76	6.2	1001	PTPX_MOUSE	P80560 mus
36	76	6.2	1132	BAT3_HUMAN	P46379 hom
37	75.5	6.2	830	VBP3_HUMAN	013488 h
38	75	6.1	199	CNTF_RABIT	P14188 oryct
39	75	6.1	315	YNEF_ECOLI	P76147 esche
40	75	6.1	343	DEPA_SYNY3	P73212 synch
41	75	6.1	450	1 TL1_DROVI	016845 dros
42	75	6.1	917	SY1_STRAU	P41972 straph
43	75	6.1	1620	ALK_HUMAN	Q9um73 hom
44	74.5	6.1	346	Y52Q_YEAST	P53259 baccha
45	74.5	6.1	409	NER1_MOUSE	035657 mus

ALIGNMENTS

RESULT 1	CTP1_RAT	STANDARD;	PRT;	203 AA.
AC	063086:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Cardiotrophin-1 (CT-1).			
GN	CTP1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
NC	NCBI_TaxID=10116;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RX	STRAIN=Miscar; TISSUE=Heart;			
RA	MEDLINE=96193659; PubMed=8604995;			
RA	Isnikawa M., Salto Y., Miyamoto Y., Kuwahara K., Ogawa E.,			
RA	Nakagawa O., Harada M., Masuda I., Nakao K.,			
RT	"CDNA cloning of rat cardiotrophin-1 (CT-1): augmented expression of			
RT	CT-1 gene in ventricle of genetically hypertensive rats.";			
RL	Biochem. Biophys. Res. Commun. 219:377-381(1996).			
CC	- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO			
CC	AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF			
CC	RECEPTOR)/GP 130 RECEPTOR COMPLEX.			
CC	- SUBCELLULAR LOCATION: Secreted (by similarity).			
CC	- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRICLE AND ATRIUM OF ADULT			
CC	RATS. ALSO DETECTED IN THE LUNG, KIDNEY, LIVER, SKELETAL MUSCLE,			
CC	STOMACH AND URINARY BLADDER. NOT DETECTED IN BRAIN, COLON, TESTIS,			
CC	SPLEEN OR THYMUS. OVEREXPRESSED IN THE VENTRICLES IN THE CASE OF			
CC	HYPERTENSION AND HYPERTROPHY.			
CC	- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; D78591; BAA11427.1; -			
DR	PIR; JC4645; JC4645.			
KW	Cytokine.			
SQ	SEQUENCE 203 AA; 21439 MW; DFB8921A2FALC832 CRC64;			
Query Match	10.2%; Score 124.5; DB 1; Length 203;			
Best Local Similarity	28.1%; Pred. No. 0.00018;			
Matches	50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;			
QY	40 IOKYTDLRRLYEHQRLAGTYLNTGPPNEBDFNPRRL---GAEFLPRATVDLEWRS 96			
DB	27 IROHNLRLRLTKRADQDLSEYVOQGEPFGSGSPRLPLAGSGAPSPAGLPV--- 83			
QY	97 LNDKRLTQNTYEAWSHLCYRLGNLQAA-----TAEIRSLAHFCTSLQGLGSIAGVM 151			

```

Db      84 ---SERLRQDDAAALGALPALLDAVRRRQKQELNPRAPRLRLSRLEDARQVRAALGAAVETVL 140
Oy      152 AALG-----PLPQPLRGTEPTPTPGPASHDFIQKXDDPFULKELOQTWLMRSKADENRL 205
      ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      141 AALGAAAGPVPPEPV-ATSALETFSNAGVFSAKYVLGLHVCGLYGBWVSRTBGDLGOL 197

RESULT 2
CTFL_MOUSE
ID_CTFL_MOUSE      STANDARD;      PRT;      203 AA.
AC      Q60753;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Cardiotrophin-1 (CT-1).
GN      CTFL.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
      [1]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=95166785; Pubmed=7862649;
RX      Pennica D., King K.L., Shaw K.J., Luis E., Rullamas J., Luo S.-M.,
RA      Dardoune W.C., Knutson D.S., Yen R., Chien K.R., Baker J.B.,
RA      Wood W.I.;
RT      "Expression cloning of cardiotrophin 1, a cytokine that induces
RT      cardiac myocyte hypertrophy.";
RL      Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).
CC      -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPY IN VITRO. BINDS TO
CC      AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
CC      RECEPTOR)/GP 130 RECEPTOR COMPLEX.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
CC      LIVER, LUNG AND KIDNEY. LOWER LEVELS IN TESTIS AND BRAIN. NO
CC      EXPRESSION IN SPLEEN.
CC      -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC      or send an email to license@isb-sib.ch).
CC
DR      EMBL; U18366; AAC52173.1; -.
DR      PIR; I49153; I49153.
DR      MGI; MGI:105115; Ctf1.
KW      Cytokine.
SQ      SEQUENCE. 203 AA; 21509 MW; 8B3D414A0B3B232F CRC64;

Query Match      9.7%; Score 118.5; DB 1; Length 203;
Best Local Similarity 28.8%; Pred. No. 0.00065;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5

Oy      40 IQKTYDILTRYDEHQRLSLAGTYLNYLGPENEPDENPRL--GAETLEPRATVDEWRS 96
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      27 IROTHNLARLLTKVAEQQLLEEVYQQGPEFGLPGPSPPRLPLAGSGPAPSHAGLPV--- 83
Oy      97 LNDKLRLLQNTVEAYSHLLCYLRGLNRQAA-----TAELRRLAHCTSLQGLISIAGYM 151
      ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      84 ---SERLRQDDAAALSVLPALLDAVRRRQKQELNPRAPRLRLSRLEDARQVRAALGAAVETVL 140
Oy      152 AALGYPV--POLPQTEPT-PTPGPASHDFIQKXDDPFULKELOQTWLMRSADENRL 205
      ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      141 AALGAAAGPVPPEPVATLTANSTAGIFSAAKVLGFHVCGLYGBWVSRTBGDLGOL 197

RESULT 3
CST_MOUSE
ID_CST_MOUSE      STANDARD;      PRT;      423 AA.
AC      Q90HE4; Q908V6;

```

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Galactosylceramide sulfotransferase (EC 2.8.2.11) (GalCer

DE sulfotransferase) (Cerebroside sulfotransferase) (3'-

DE phosphoadenylylsulfate:galactosylceramide 3'-sulfotransferase)

DE (3'-phosphoadenylylsulfate:5'-phosphosulfate:GalCer sulfotransferase).

GN Cst OR CGST.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC TISSUE=Kidney;

RC MEDLINE=20193614; PubMed=10727929;

RA Hirahara Y., Tsuda M., Wada Y., Honke K.;

RT "cDNA cloning, genomic cloning, and tissue-specific regulation of

RT cerebroside sulfotransferase."

RL Eur. J. Biochem. 267:1909-1917(2000).

RL [2]

RN SEQUENCE FROM N.A.

RP STPAIN=C57BL/6J; TISSUE=Pancreas;

RC MEDLINE=21085660; PubMed=11219511;

RX Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Atakawa T., Hara A., Fukunishi Y., Komo H., Aachi S., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,

RA Sato T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischman M., Gaasterland T., Gissi C., King B., Koehli H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schirral L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberte P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Yuzhakov-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

RN [3]

RN SEQUENCE FROM N.A.

RP TISSUE=Colon;

RC MEDLINE=22386257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Gronow L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschuler S.F., Ziegler B., Buetow K.H., Scheffer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marsina K., Farmer A.S., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange S.J.,

RA Rana S.S., Loquellano N.A., Peters S.J., Abramson R.D., Mullaly S.C.,

RA Bosak S.A., Mcwan P.J., McEran K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [4]

RN FUNCTION.

RP MEDLINE=1927584; PubMed=11917099;

RA Honke K., Hirahara Y., Dupree J., Suzuki K., Popko B., Fukushima K.,

RA Fukushima J., Nagasawa T., Yoshida N., Wada Y., Taniguchi N.;

RT "Paranodal junction formation and spermatogenesis require
 RT sulfolipolipids.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4227-4232(2002).
 CC -1- FUNCTION: Catalyzes the sulfation of membrane glycolipids. Seems
 CC to prefer beta-glycosides at the nonreducing termini of sugar
 CC chains attached to a lipid moiety. Catalyzes the synthesis of
 CC HSO3-3-galactosylceramide (sulfatide), a major lipid component of
 CC the myelin sheath and of HSO3-3-monoalactosylglycerol
 CC (smonolipid), present in spermatocytes. Also acts on
 CC lactosylceramide, galactosyl 1-alkyl-2-en-glycerol and galactosyl
 CC diacylglycerol (in vitro).
 CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a
 CC galactosylceramide = adenosine 3',5'-bisphosphate +
 CC galactosylceramide sulfate.
 CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate +
 CC monoalactosylglycerol = adenosine 3',5'-bisphosphate +
 CC monoalactosylglycerol sulfate.
 CC -1- PATHWAY: sphingolipid and glycerolipid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in brain, testis, kidney, stomach,
 CC small intestine, liver, and lung. Not detected in heart, skeletal
 CC muscle, and spleen.
 CC -1- MISCELLANEOUS: Mice homozygous for a null mutation of the CST gene
 CC display hindlimb weakness from week 6 of age and subsequently show
 CC a pronounced tremor and progressive ataxia. Myelin vacuolation is
 CC observed in the cerebellar white matter, diencephalon, brainstem
 CC and spinal anterior column. Male mice were infertile due to a
 CC blocked spermatogenesis.
 CC -----
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 CC -----
 CC DR EMBL, AB032940; BAA93009.1; -;
 CC DR EMBL, AB032939; BAA93008.1; -;
 CC DR EMBL, AK007645; BAB25160.1; -;
 CC DR EMBL, BC026806; AAB26806.1; -;
 CC DR MGD, MGI:1858277; Gcat.
 CC DR GO, GO:0016021; C:integral to membrane; IC.
 CC DR GO, GO:0001733; F:galactosylceramide sulfoltransferase activity; IDA.
 CC DR GO, GO:0006682; F:galactosylceramide biosynthesis; IDA.
 CC DR GO, GO:0042552; P:myelination; IMP.
 CC DR GO, GO:0007283; P:spermatogenesis; IMP.
 CC KW Transferase; Transmembrane; Glycoprotein.
 CC PT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
 CC PT TRANSMEM 13 35 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC PT (POTENTIAL).
 CC PT DOMAIN 36 423 LUMENAL, CATALYTIC (POTENTIAL).
 CC PT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC PT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC PT CONFLICT 18 18 L -> P (IN REF. 2).
 CC PT CONFLICT 263 263 R -> Q (IN REF. 2).
 CC PT CONFLICT 271 271 E -> K (IN REF. 2).
 CC PT CONFLICT 358 358 Q -> R (IN REF. 1).
 CC PT CONFLICT 392 392 R -> G (IN REF. 2).
 CC PT CONFLICT 398 398 I -> T (IN REF. 1).
 CC SQ SEQUENCE 423 AA, 48968 MW, PDS4A1A71F4ABE46 CRC64;
 CC
 CC Query Match 7.7%; Score 94; DB 1; Length 423;
 CC Best Local Similarity 22.7%; Pred. No. 0.31;
 CC Matches 55; Conservative 23; Mismatches 60; Indels 104; Gaps 12;
 CC
 CC 44 YDLTYLLEHQAASLACTYANTY---LGPP-----FNP----- 72
 CC 204 YDPSSNAHYNLNLLFPDGLGYSSLDPPASPRVOEHLEVERPHVLQGEYVDESILVLR 263
 CC 73 -----DFNPPRLGAGETLPRAT-----VDEWRSLSLNDKRLTONVEA 109

Db 264 ELTCWDLDEVLVFKLNARSDSPVRLSGELYRATANWLLDVRLYHFN--ASFWRKYEA 321
 Qy 110 YSHLCTYRGINRQA-ATAEIIRS---LAHCTSLQGLLGSTA-----GWMA 153
 Db 322 F-----GGRMRREVAELRQANEHRHCTIDGQAVGABAIQDSAMPQPIGIST 373
 Qy 154 LGYPLPQPLPTEPTPTWTPGPHSDPLQKMDFFWLKELQ-----TWLMSAKDF 202
 Db 374 LGVNYAKSI-----GPGHEQLCRM-----LTPEIQYSLDGLANLWTKWFLADF 420
 Qy 203 NR 204
 Db 421 LR 422
 RESULT 4
 ID NXF1_HUMAN STANDARD; PRT; 619 AA.
 AC Q9UBU9; Q99799; Q9UOL2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Nuclear RNA export factor 1 (TAP associating protein) (TAP-associated
 DE protein) (mRNA export factor TAP).
 GN NXF1 OR TAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.
 RC TISSUE=Cervical carcinoma.
 RX MEDLINE=99219873; PubMed=10202158;
 RA Braun I.C., Rohrbach E., Schmitt C., Izaurralde E.;
 RT "TAP binds to the constitutive transport element (CTE) through a novel
 RT RNA-binding motif that is sufficient to promote CTE-dependent RNA
 RT export from the nucleus.";
 RL EMBO J. 18:1953-1965(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99257272; PubMed=10323864;
 RA Kang Y., Cullen B.R.;
 RT "The human TAP protein is a nuclear mRNA export factor that contains
 RT novel RNA-binding and nucleocytoplasmic transport sequences.";
 RL Genes Dev. 13:1126-1139(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99384298; PubMed=10454577;
 RA Bear J., Tan W., Zolotukhin A.S., Taberner C., Hudson E.A.,
 RA Felder B.K.;
 RT "Identification of novel import and export signals of human TAP, the
 RT protein that binds to the constitutive transport element of the type
 RT D retrovirus RNAs.";
 RL Mol. Cell. Biol. 19:6306-6317(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner C.M., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
 RA Brownstein M.J., Ueiri T.B., Toshiyuki S., Carinici P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muljany S.J.,
 RA Boeck S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marx M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
 RA Ohtsuka T., Sugano S.;
 RA "NEO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 61-619 FROM N.A.
 RC TISSUE=Lymphocytes;
 RA MEDLINE=97318898; PubMed=9175835;
 RA Yoon D.-W., Lee H., Seol W., Demaria M., Rosenzweig M., Jung J.U.;
 RT "Tap: a novel cellular protein that interacts with tip of herpesvirus
 RT salivari and induces lymphocyte aggregation."; Immunity 6:571-582(1997).
 RN [7]
 RP FUNCTION.
 RA MEDLINE=98325379; PubMed=9660949;
 RA Grueter P., Taberner C., von Kobs C., Schmitt C., Saavedra C.,
 RA Bachl A., Wilm M., Felder B.K., Izaurralde E.;
 RT "TAP, the human homolog of Mex67p, mediates CTE-dependent RNA export
 RT from the nucleus."; Mol. Cell 1:649-659(1998).
 RN [8]
 RP CHARACTERIZATION.
 RA MEDLINE=21282872; PubMed=11259411;
 RA Braun I.C., Herold A., Rode W., Conti E., Izaurralde E.;
 RT "Overexpression of TAP/p15 heterodimers bypasses nuclear retention and
 RT stimulates nuclear mRNA export."; J. Biol. Chem. 276:20536-20543(2001).
 RN [9]
 RP CHARACTERIZATION.
 RA MEDLINE=20132240; PubMed=1066806;
 RA Bachl A., Braun I.C., Rodriguez J.P., Pante N., Ribbeck K.,
 RA von Kobs C., Kutay U., Wilm M., Gorlich D., Carmo-Fonseca M.,
 RA Izaurralde E.;
 RT "The C-terminal domain of TAP interacts with the nuclear pore complex
 RT and promotes export of specific CTE-bearing RNA substrates."; RNA 6:136-158(2000).
 RN [10]
 RP MUTAGENESIS.
 RA MEDLINE=21151125; PubMed=11256625;
 RA Suyama M., Doerks T., Braun I.C., Sattler M., Izaurralde E., Bork P.;
 RT "Prediction of structural domains of TAP reveals details of its
 RT interaction with p15 and nucleoporins."; EMBO Rep. 1:53-58(2000).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 102-372.
 RA MEDLINE=20514125; PubMed=11060011;
 RA Liker E., Fernandez E., Izaurralde E., Conti E.;
 RT "The structure of the mRNA export factor TAP reveals a cis arrangement
 RT of a non-canonical RNP domain and an LRR domain."; EMBO J. 19:5587-5598(2000).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH NXT1, AND X-RAY
 RP CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH NXT1-FG-REPEAT.
 RA MEDLINE=21468398; PubMed=11583626;
 RA Fribourg S., Braun I.C., Izaurralde E., Conti E.;
 RT "Structural basis for the recognition of a nucleoporin FG repeat by
 RT the NTF2-like domain of the TAP/p15 mRNA nuclear export factor."; Mol. Cell 8:645-656(2001).
 RN [13]
 RP STRUCTURE BY NMR OF 551-619, AND MUTAGENESIS OF PHE-617.
 RA MEDLINE=21912422; PubMed=11875519;
 RA Grant R.P., Hurt E., Neuhaus D., Stewart M.;

RT "Structure of the C-terminal FG-nucleoporin binding domain of
 RT Tap/NXF1."; Nat. Struct. Biol. 9:247-251(2002).
 RN [14]
 RP FUNCTION: Involved in the nuclear export of mRNA species bearing
 CC retroviral constitutive transport elements (CTE) and in the export
 CC of mRNA from the nucleus to the cytoplasm.
 CC -1 SUBUNIT: Interacts with NXT1, NXT2, E1B-AP5, RAE1, the REF
 CC proteins and with several nucleoporins.
 CC -1 SUBCELLULAR LOCATION: Nuclear; localized predominantly in the
 CC nucleoplasm and at both the nucleoplasmic and cytoplasmic foci of
 CC the nuclear pore complex. Shuttles between the nucleus and the
 CC cytoplasm.
 CC -1 TISSUE SPECIFICITY: Expressed ubiquitously.
 CC -1 DOMAIN: The minimal CTE binding domain consists of an RNP-
 CC type RNA binding domain (RBD) and leucine-rich repeats.
 CC -1 DOMAIN: The nucleoporin binding domain consists of a NTF2-like
 CC domain and a UBA-like domain. The NTF2 domain heterodimerizes with
 CC NXT1 AND NXT2. The formation of NXF1/NXT1 heterodimers is required
 CC for NXF1-mediated nuclear mRNA export. The UBA-like domain
 CC mediates direct interactions with nucleoporin-FG-repeats and is
 CC necessary and sufficient for localization of NXF1 to the nuclear
 CC rim. The conserved loop 594-NMD-596 of the UBA domain has a
 CC critical role in the interaction with nucleoporins.
 CC -1 DOMAIN: The leucine-rich repeats and the NTF2-domain are
 CC essential for the export of mRNA from the nucleus.
 CC -1 MISCELLANEOUS: The RNA-binding domain is a non-canonical RNP-type
 CC domain.
 CC -1 SIMILARITY: BELONGS TO THE NXF FAMILY.
 CC -1 SIMILARITY: Contains 4 leucine-rich (LRR) repeats.
 CC -1 SIMILARITY: Contains 1 NTF2 domain.
 CC -1 SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1 SIMILARITY: Contains 1 UBA-like domain.
 CC
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 CC
 CC EMBL; AJ132712; CAA10753.1; -
 CC EMBL; AF112880; AAD39102.1; -
 CC EMBL; AF126246; AAD20016.1; -
 CC EMBL; BC004904; AAH04904.1; -
 CC EMBL; AK027192; -, NOT_ANNOTATED_CDS.
 CC EMBL; U80073; AAB81111.1; -
 CC PDB; 1F01; 03-NOV-00.
 CC PDB; 1FT8; 11-DEC-00.
 CC PDB; 1KOH; 27-FEB-02.
 CC PDB; 1KOO; 27-FEB-02.
 CC PDB; 1OAT; 20-FEB-03.
 CC Gene; HGNC:8071; NXF1.
 CC GK; Q9UBU9; -
 CC MIM; 602647; -
 CC InterPro; IPR001611; LRR.
 CC InterPro; IPR003603; LRRcap.
 CC InterPro; IPR002075; NTF2.
 CC InterPro; IPR005637; TAP_C.
 CC PDB; 1G05; 28-MAR-02.
 CC PDB; 1JUG; 18-DEC-02.
 CC PDB; 1JN5; 23-JUL-01.
 CC Pfam; PF00560; LRR; 1.
 CC Pfam; PF02136; NTF2; 1.
 CC Pfam; PF03943; TAP_C; 1.
 CC PRINTS; PR00019; LEURICHRP.
 CC SMART; SM00446; LRRcap; 1.
 CC PROSITE; PS0177; NTF2_DOMAIN; 1.
 CC Transport; mRNA transport; Nuclear protein; RNA-binding; Repeat;
 CC Leucine-rich repeat; Multigene family; 3D-structure.
 CC DOMAIN 119 198 RNA-BINDING (RRM).
 FT

Query Match

7.6%; Score 93; DB 1; Length 619;

Best Local Similarity 24.7%; Pred. No. 0.63;
Matches 60; Conservative 32; Mismatches 93; Indels 58; Gaps 13;

QY 5 AGDSWGM-----ALCTVYMLPVPALNRTGDP-GGSPISQKTYDIT---RYLEHOL 54
DB 400 SGGROGLLAVHDACCSTIPETPNPAPSSIAETFKOSRNKKDKDPLRPRLLKHTR 459
QY 55 RSLACTVLYLVGPPFPPNP--PRLAGETLPRATVDL-----EYWRSLNDKLR-LTON 106
DB 460 LNVV-AFLNEL--PKQHDVNSFVVDISAQSTLLCPNSVNGVKEDGSRDRLAFTRT 516
QY 107 Y---EAYSHLLCYLRG-LNRQATATLRRSLAHFCTSLQGLGSIAGVMAALGYPLPOP 161
DB 517 FIAVPASNSGLCTIVNDELFRVNASSEIQRAFA-----MPAP 553
QY 162 LPCTETPTWPPGPHSPFLQK-----MDDFWLKEIQTWIM---RSAXDPNRLKKKKMOP 212
DB 554 TPSSSVFPTLSPQOEMLOAFSTQSGMNLWESQKCLQDNNWDYTRSAQAFTHLKAGEIP 613
QY 213 AAA 215
DB 614 EVA 616

RESULT 5
CTFL_HUMAN STANDARD; PRT; 201 AA.
AC 016619;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardiotoxin-1 (CT-1).
GN CTFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=96429882; PubMed=8833032;
RA Pennica D., Swanson T.A., Shaw K.J., Kuang W.-J., Gray C.L.,
RA Beatty B.G., Wood W.I.;
RT "Human cardiotoxin-1: protein and gene structure, biological and
RT binding activities, and chromosomal localization.";
RL Cytokine 8:183-189(1996).
CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
CC RECEPTOR)/gp 130 RECEPTOR COMPLEX.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
CC PROSTATE AND OVARY. LOWER LEVELS IN LUNG, KIDNEY, PANCREAS,
CC THYMUS, TESTIS AND SMALL INTESTINE. LITTLE OR NO EXPRESSION IN
CC BRAIN, PLACENTA, LIVER, SPLEEN, COLON OR PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL; U43033; AAD12173.1; -
CC EMBL; U43033; AAD12173.1; JOINED.
CC EMBL; U43033; AAD12173.1; JOINED.
CC EMBL; U43033; AA85223.1; -
CC PIR; G02312; G02312.
CC GeneW; HGNC:2499; CTFL.
CC MIM; 600435; -
CC GO; GO:0005576; C:extracellular; TAS.

DR GO; GO:0005146; F:leukemia inhibitory factor receptor ligand . . .; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007517; P:muscle development; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
KW Cytokine; Polymorphism.
FT VARIANT 92 92 A -> T (IN dbSNP:2234933).
FT FTID=VAR 014938.
SQ SEQUENCE 201 AA, 21227 MW, 0235A7B5745F875F CRC64;
Query Match 7.5%; Score 91.5; DB 1; Length 201;
Best Local Similarity 25.9%; Pred. No. 0.21;
Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;

QY 40 IOKTDLRYLEHOLRSLAGTYLANTLVGPPFPPNPRLAGETLPRATVDLEWRSLND 99
DB 27 IROTSLHLTLTKVAEQQLQEVYQIQGDPFGLPSPSPRLPVAGL-SAPAPSHAGLPVHE 85
QY 100 KRLTONYEAVSHLLCYLRGLNRQA-----TAEFRSLAHFCTSLQGLGSIAGVMAAL 154
DB 86 RLRL--DAALALAPPLDVCRRQASLNPRAPRLRLRLEDAARALGAAYVALLNAL 143
QY 155 GYPLPQPLPGTER--TWTPGPHSDPLQKDDFWLKEIQTWIMRSKDFNRL 205
DB 144 G--AANRGPRAPPAATASASATGVPPAKVIGLRVGVYRWLRTSGDLQGL 195

RESULT 6
HAIR_MOUSE STANDARD; PRT; 1182 AA.
AC 061645;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hairless protein.
GN HR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Skin;
RX MEDLINE=94329587; PubMed=8052649;
RA Cachon-Gonzalez M.B., Fenner S., Coffin J.M., Moran C., Best S.,
RA Stoye J.P.;
RT "Structure and expression of the hairless gene of mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).
CC -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO
CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN, HAIR
CC FOLLICLES AND INTERFOLLICULAR EPIDERMIS. NO EXPRESSION IN
CC DERMIS.
CC -1- DISEASE: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS
CC INCLUDING STRUCTURAL ABNORMALITIES OF EPITHELIAL CELLS IN THE HAIR
CC FOLLICLES, HAIR LOSS TOWARDS THE END OF THE FIRST HAIR GROWTH
CC CYCLE, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER
CC MICE CARRYING AN HR MUTATION HAVE BEEN REPORTED TO POSSESS ALTERED
CC RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMOZYGOUS FOR
CC HR MUTATION ARE UNIQUELY SENSITIVE TO UV AND CHEMICALLY INDUCED
CC SKIN TUMORS.
CC -----
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CC -----
CC EMBL; Z32675; CAA83587.1; -

DR PIR; 148378; 148378.
 DR MGD; MGI:96223; hr.
 DR InterPro; IPR003347; TF_JmJC.
 DR Pfam; PF02373; JmJC; 1.
 DR SMART; SM00558; JmJC; 1.
 DR Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
 KW Metal-binding.
 FT ZN FING 595 620 C6-TYPE.
 FT ZN FING 535 540 POLY-GLY.
 FT DOMAIN 535 540 POLY-GLY.
 SQ SEQUENCE 1182 AA; 127182 MW; BFBDBE62ABE1B40 CRC64;
 Query Match 7.5%; Score 91.5; DB 1; Length 1182;
 Best Local Similarity 23.7%; Pred. No. 2;
 Matches 70; Conservative 25; Mismatches 99; Indels 101; Gaps 17;
 QY 3 LRAGSGMGLACTCTVLMPLPAVPALNRTGDPG-----PPG----- 38
 DB 813 LRAGS--GIRKGL-----SLPSPVTRTLPSPGALLMLOEPPRKGFHLEQEHWRQGPV 865
 QY 39 ---SIQKTYDLTRYLEHQRLSLAGTY--LNYLGGP-----FNEEDFNPRLG 80
 DB 866 LVSGIQTIRLRLSLMGHEALGTIGQVQITLALGPPTMLDSTAWEGSHETRP----- 921
 QY 81 AETLPRAVYDLEWRSGLNDK-LRLTON-----YEAVSHLLCYL-RGLNRQAT 126
 DB 922 --KLDEGSV-LIHRTLGDKDASRVQNLASLPLEYCAHQKGLNLAFLPLGLTHPLE 978
 QY 127 AEL-----RSLAHFCTSLQGLLGSAGVMAALGYLPPLPPTETPTTPGPAH 175
 DB 979 POLMAAYGVNHRHGLGTNNLCVEVSDLSILVHAEOI-----PPWY--RAQ 1024
 QY 176 SDFLOKMD--DFWLKELOTWLMR--SAKDFNRLKKKQP--PAAAVTLHLGAG 224
 DB 1025 KDFLSGLDGEGLMSGSGSTVWVHFRADQAIRIRFLQWCPAGATLEPARG 1079
 RESULT 7
 CNTF_CHICK STANDARD; PRT; 195 AA.
 AC 002011;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Ciliary neurotrophic factor (CNTF) (Growth promoting activity) (GPA).
 OS CNF OR GPA.
 GN Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92304573; PubMed=1610564;
 RA Leung D.W., Parent A.S., Cachianes G., Lee A.L., Nikolic K.,
 RA Esch F., Coulombe J.N., Blacher R.W., Eckenstein F.P., Nishi R.,
 RA "Cloning, expression during development, and evidence for release of
 RA a trophic factor for ciliary ganglion neurons.",
 RL Neuron 8:1045-1053(1992).
 CC - FUNCTION: CNTF IS A SURVIVAL FACTOR FOR VARIOUS NEURONAL CELL
 CC TYPES. SEEMS TO PREVENT THE DEGENERATION OF MOTOR AXONS AFTER
 CC AXOTOMY.
 CC - SUBCELLULAR LOCATION: Cytoplasmic.
 CC - TISSUE SPECIFICITY: NERVOUS SYSTEM.
 CC - SIMILARITY: BELONGS TO THE CNTF FAMILY.
 CC -----
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 CC -----

DR EMBL; M80827; AAA8784.1; -
 DR PIR; JH0680; JH0680.
 DR HSSP; P26441; ICNTF.
 DR InterPro; IPR000151; C11_neuro_factor.
 DR Pfam; PF01110; CNTF; 1.
 DR ProDom; PD011041; C11_neuro_factor; 1.
 KW Growth factor; Neuron.
 SQ SEQUENCE 195 AA; 21330 MW; FEA076949DB34ACS CRC64;
 Query Match 7.4%; Score 91; DB 1; Length 195;
 Best Local Similarity 27.3%; Pred. No. 0.22;
 Matches 51; Conservative 21; Mismatches 83; Indels 32; Gaps 9;
 QY 46 LTRYEHQRLSLAGTYLNYLVLPPEFNEPFPNPRGLAETLPATVDFEWRSLNDKRLTQ 105
 DB 23 LARKRSVTDLLDIYVRQG-----LDASISVAADVGPTRAAV--EKMAQGTQRLID 75
 QY 106 N---YEAVSHLLCYLRLNROA--ATAELRRSLA-----HFCTSLQGLLGSAGVMA 152
 DB 76 NLAAVRAVTRTLLAQMLEQRELLGDTDAELGPALAAMLQVSAPVYHLBEIL-----ELE 130
 QY 133 ALGYLPPLPPTETPTTPGPAH--SDFLOKMDDFWLKELOTWLMRSKADFNRLKKKQP 211
 DB 131 SRGAPAEH---GSEP---PAPPRSLFPOKRLGRLVRELAQMAVRSVDRLOLSKQPG 184
 QY 212 PAAAVTL 218
 DB 185 SGALGL 191
 RESULT 8
 MIP1_SCHPO STANDARD; PRT; 1313 AA.
 ID MIP1_SCHPO
 AC P87141;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE WD-repeat protein Mip1 facilitates function of the meiotic
 GN WD-repeat protein mip1.
 OS MIP1 OR SPAC57A7.11.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=20115869; PubMed=10648609;
 RA Shinozaki-Yabana S., Watanabe Y., Yamamoto M.,
 RA "Novel WD-repeat protein Mip1 facilitates function of the meiotic
 RA regulator Mei2p in fission yeast.",
 RL Mol. Cell. Biol. 20:1234-1242(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Wolckart G., Aert R., Robben J., Gymnopoulos B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel K., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Bozzym K., Langer I., Beck A., Leirich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Weiler H., Wambolt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galbert F., Avea S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucie M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revelante J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*,"
 RL Nature 415:871-880(2002).
 CC -1- REGULATOR BINDS TO AND FACILITATES THE FUNCTIONING OF THE MEIOTIC
 CC WITH STREII. ESSENTIAL FOR CELL GROWTH.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Contains 7 WD repeats.
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 CC
 CC EMBL, AB03552; BAA84585.1; -
 CC EMBL, Z55336; CAB08769.1; -
 CC PIR, T38943; T38943.
 CC GenBank, SPMB06; SPAC57A7.11; -
 CC InterPro: IPR001680; WD40.
 CC InterPro: IPR004083; YeastC176.
 CC Pfam, PF00400; WD40; 5.
 CC PRINTS, PR01547; YEAST176DUF.
 CC SMART, SM00320; WD40; 6.
 CC PROSITE, PS00678; WD_REPEATS_1; 1.
 CC PROSITE, PS50082; WD_REPEATS_2; 2.
 CC PROSITE, PS50294; WD_REPEATS_REGION; 1.
 CC Metastats; WD repeat; Repeat.
 KW Metastats; WD repeat; Repeat.
 FT REPEAT 966 1029 WD 1.
 FT REPEAT 1033 1074 WD 2.
 FT REPEAT 1087 1126 WD 3.
 FT REPEAT 1130 1170 WD 4.
 FT REPEAT 1176 1216 WD 5.
 FT REPEAT 1219 1259 WD 6.
 FT REPEAT 1268 1308 WD 7.
 FT REPEAT 1313 1353 WD 7.
 SQ SEQUENCE 1313 AA; 148533 MW; C71B63B0171E7A4 CRC64;
 Query Match 7.3%; Score 89.5; DB 1; Length 1313;
 Best Local Similarity 22.8%; Pred. No. 3.5;
 Matches 61; Conservative 32; Mismatches 69; Indels 105; Gaps 14;
 QY 15 LCTVLMHLPAV--PALNR-----TGDPGPGPSI-----OKTYDLTRYLEHQRSS 56
 DB 811 LAFLLQHLPALMKASLSKDTNSVTSDDKPHFPVPSVSEKILNRSPLTSLKGLALS 870
 QY 57 LAG-----TYLNYL-----GPP-FNEPDPNPRLCAETLPPATYDL 91
 DB 871 LAGSRASELSLINSKPKASBNLNLTSAKVGPAPAFNELEY-----QSEIDM 919
 QY 92 EWRRLND-----KRLTONYEAYSHLLCYLGL--NRQATAELRLSLAHFCTS 139
 DB 920 PLTSTYLFDMRSRYFTPEPQRPNEDEPGS--ICYNQRLMRNRNREKLIYRTPLALEYSTN 977
 QY 140 -----LQGLLSIAGVMAALGYPLPQLPGTEPTWTPGPAHSDFLQKMDPWLKE-- 190
 DB 978 GRMNOQLMTFNNTIA-----PRLTMHQPEDDQITIGDDXI 1013
 QY 191 LQTLWLRSAKDPNRLKKQKQPPAAVLT 217
 DB 1014 IQVMDMRR-----NRCINSEKTSASAT 1036
 RESULT 9
 HAIR_RAT STANDARD; PRT; 1181 AA.
 AC P97609;

DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Hairless protein.
 GN HR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=97141510; PubMed=8987811;
 RA Thompson C.C.;
 RT "Thyroid hormone-responsive genes in developing cerebellum include a
 RT novel synaptotagmin and a hairless homolog.";
 RL J. Neurosci. 16:7832-7840(1996).
 CC -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO
 CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
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 CC
 CC EMBL, U71293; AAC53018.1; ALT_INIT.
 CC InterPro: IPR003347; TF_JmJC.
 CC Pfam, PF02373; JmJC; 1.
 CC SMART, SM00558; JmJC; 1.
 CC Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
 KW Metal-binding.
 FT ZN FING 594 619 C6-TYPE.
 FT ZN FING 1181 AA; 127307 MW; 834B7029CF8E89F0 CRC64;
 SQ SEQUENCE 1181 AA; 127307 MW; 834B7029CF8E89F0 CRC64;
 Query Match 7.1%; Score 87.5; DB 1; Length 1181;
 Best Local Similarity 25.3%; Pred. No. 4.6;
 Matches 61; Conservative 21; Mismatches 92; Indels 67; Gaps 12;
 QY 30 RTGDPGPGPSIOKTYDLTRYLEHQRSLAGTY--LNYVGGP-----FNEPDF 74
 DB 859 RQGPVYVSGIQKTLRLSLMGEBALGTIGGOVOTITLGPPOPTSLDSTAFKFSHEA 918
 QY 75 NPPRLGAEPLPRATVDLEWRSINDK-----LRLTQ-----NYEAYSHLLC 115
 DB 919 RP-----KLDEGSV-LILHRLPLDGDKDSRVENLASSLPLEVCYAHQKMLNLSVLPGL 971
 QY 116 YLRGLNRQAATLRLRS-----LAHFCTSLQGLLSIAGVMAALGYPLPOPLPETPTW 169
 DB 972 TLHPLEPQLMAAYGVNSHRGHGKTNLCVEVSDLSILVHAEAOL-----PPW 1019
 QY 170 TPGPAHSDFLQKMD--DPWLKELQITWLMR--SAKDFNRLKKQKP--PAAAVTLHLGAH 223
 DB 1020 Y--RQKQDFLSGLGBGLMSGSGSTSTVWYHVPKQDAQIRKIRFLQMVCPAGAGTLEPAP 1077
 QY 224 G 224
 DB 1078 G 1078
 RESULT 10
 M2B2_HUMAN
 ID M2B2_HUMAN STANDARD; PRT; 1009 AA.
 AC Q9Y2E5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Epididymis-specific alpha-mannosidase precursor (EC 3.2.1.24)
 DE (Mannosidase alpha class 2B member 2).
 GN MAN2B OR KIAA0935.

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ciliary neurotrophic factor (CNTF).
 GN CNTF.
 OS *Sus scrofa* (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 NCBI_TaxID:9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98030048; PubMed=9363597;
 RA Weaks R.L., Ramsondar J.J., Gallagher D.S. Jr., Nogues C.,
 RA Piedrahita J.A.;
 RT "Isolation, characterization and chromosomal localization of the
 RL porcine ciliary neurotrophic factor (CNTF) gene.";
 RL *Anim. Genet.* 28:354-357(1997).
 CC -1- FUNCTION: CNTF IS A SURVIVAL FACTOR FOR VARIOUS NEURONAL CELL
 CC TYPES. SEEMS TO PREVENT THE DEGENERATION OF MOTOR AXONS AFTER
 CC AXOTOMY (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CNTF FAMILY.
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 CC -----
 DR EMBL: U57644; AAC27342.1; -
 DR HSP: P26441; 1CNT.
 DR Interpro: IPR000151; C11_neuro_factor.
 DR Pfam: PF01110; CNTF; 1.
 DR Prodom: PD011041; C11_neuro_factor; 1.
 DR Growth factor: Neurope.
 SQ SEQUENCE 200 AA; 22718 MW; 40507C4457ED6531 CRC64;
 Query Match 6.9%; Score 84; DB 1; Length 200;
 Best Local Similarity 24.7%; Pred. No. 1;
 Matches 47; Conservative 23; Mismatches 88; Indels 32; Gaps 9;
 QY 46 LRRYLEHQRSLAGTLANLGPPRPDPNPPRLGAEITPRATVDLEVRSLNDKRLQ 105
 DB 23 LARKRSDDLALMEAVYKQG--LNF---NINLDVGVPMASDTR--VSELTAEERLQ 75
 QY 106 NTEAVSHLLCYLRGLNRQATAELRSLAHFCTS---LQGLGSLGVAALGYPLPQ-- 160
 DB 76 NLRATYTRHVMRL-----LEQREHFTPAEDDFHOAHITTVLQVAAFRYQLEELM 127
 QY 161 -----PLPTEPTPTGPAHSD--FLQKNDFFWLKELQTWLRSKDNRLKKKKQPPA 213
 DB 128 VLEHKKVPSEADGTPLVGGGGLFKKLMGLVQLGELSQWTVRSIRDLRVISSHQ----- 183
 QY 214 AAVTLHLGHN 223
 DB 184 AGVPAH-GSH 192
 RESULT 13
 TIL_DROME
 ID TIL_DROME STANDARD; PRT; 452 AA.
 AC P18102; O9VA33;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tailless protein.
 GN TIL OR NR2E2 OR CG1378.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=90304905; PubMed=2364433;
 RA Pignoni F., Balderelli R.M., Steingrimsson E., Diaz R.J.,
 RA Patapoutian A., Merriam J.R., Lengyel J.A.;
 RT "The *Drosophila* gene *tailless* is expressed at the embryonic termin
 RL and is a member of the steroid receptor superfamily.";
 RL *Cell* 62:151-163(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93157371; PubMed=8430097;
 RT Liao G.-J., Steingrimsson E., Pignoni F., Couray A.J., Lengyel J.A.;
 RL "Characterization of downstream elements in a Raf-1 pathway.";
 RL *Proc. Natl. Acad. Sci. U.S.A.* 90:858-862(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutcliffe G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaslev E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borrova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Fabios B., DeJocher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doug L.E., Downes M., Dugan-Hoch S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.U., Mei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimnos I., Simpson M., Skupski M.P., Smith T.,
 RA Spiers E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitkay R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL *Science* 287:2185-2195(2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=99287803; PubMed=10357938;
 RA Daniel A., Dumattei K., Lengyel J.A., Hartenstein V.;
 RT "The control of cell fate in the embryonic visual system by atonal,
 RT *tailless* and *EGFR* signaling.";
 RL Development 126:2945-2954(1999).
 CC -1- FUNCTION: ORPHAN RECEPTOR THAT BINDS DNA AS A MONOMER TO HORMONE
 CC SITE SEQUENCE 5'-AATCA-3' IN WHICH THE 5' FLANKING NUCLEOTIDES
 CC PARTICIPATE IN DETERMINING RECEPTOR SPECIFICITY. THIS RECEPTOR
 CC BINDS TO THE CONSENSUS SEQUENCE (AG) (AG)AATCA. PLAYS A KEY ROLE
 CC IN THE ESTABLISHMENT OF NONMERAMERIC DOMAINS AT THE ANTERIOR AND
 CC POSTERIOR POLES OF THE EMBRYO. IT MAY ALSO PLAY A ROLE IN THE
 CC NERVOUS SYSTEM. THE MATERNAL TERMINAL PATHWAY ACTIVATES THE TIL


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CC GENE IN THE TERMINI, TEL ACTIVITY THEN REPERSES SEGMENTATION AND
CC ACTIVATES TERMINAL-SPECIFIC GENES IN THESE DOMAINS. INVOLVED IN
CC THE REGULATION OF EARLY EYE DEVELOPMENT. IN THE EMBRYONIC VISUAL
CC SYSTEM ANTAGLE DRIVES CELLS TO OPTIC LOBE AS OPPOSED TO BOWLING/S
CC ORGAN FATE.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL NERVOUS SYSTEM.
CC -1- DEVELOPMENTAL STAGE: DURING STAGE 10 FOUND IN THE ANTERIOR PART OF
CC THE VISUAL SYSTEM THAT LATER GIVES RISE TO THE ANTERIOR LIP OF THE
CC OPTIC LOBE. AT STAGE 12 ALSO FOUND IN THE POSTERIOR LIP OF THE
CC OPTIC LOBE. IN THIRD LARVAL INSTAR EXPRESSED IN THE OPTIC LOBE OF
CC THE LARVAL BRAIN AND IN THE EYE ANTENNAL DISK, BOTH IN ANTENNAL
CC AND EYE PORTION.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34639; AAA28936.1; -
DR EMBL; AF019362; AAB71371.1; -
DR EMBL; AE003775; AAF57091.1; -
DR PIR; A35602; A35602.
DR HSSP; P10826; 1HRA:
DR TRANSFAC; T00789; -
DR FLYBase; FBgn0005720; t11.
DR GO; GO:0007369; P:gastulation; NAS.
DR GO; GO:0007362; P:terminal region determination; IGI.
DR GO; GO:0008293; P:torso receptor signaling pathway; IGI.
DR InterPro; IPR000536; Hormone rec lig.
DR InterPro; IPR001723; Strchnm_receptor.
DR InterPro; IPR001628; Znf_Casteroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHOMOMER.
DR PRINTS; PR00047; STROIDFINGER.
DR PRODOM; PD000035; Znf_Casteroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Activator; Repressor; Developmental protein..
FT DNA_BIND 34 101 NUCLEAR RECEPTOR-TYPE.
FT FT 34 101
FT ZN_FING 34 54 C4-TYPE.
FT ZN_FING 70 96 C4-TYPE.
FT FT 244 389 LIGAND-BINDING (BY SIMILARITY).
FT DOMAIN 262 265 POLY-LEU.
SO SEQUENCE 452 AA; 50549 MW; AABBFED93A37C CMC64;

Query Match 6.8%; Score 83; DB 1; Length 452;
Best Local Similarity 23.8%; Pred. No. 3.6;
Matches 34; Conservative 11; Mismatches 32; Indels 66; Gaps 6;

QY 115 CYLGILNRQATAE-----LRSLIAFCTSLQGLIAGTGM-----AALG 155
Db 96 CFEVGNMNDVAOHERGPRNSTLRHMAYKQAMMG-----AGEMFQIPAEIIMNTAALTG 150
QY 156 YP-LPOLPTEPTWTPGPAHSDFLOKDDFWLKELOTWLMRSKADFNRLKKKQPPAA 214
Db 151 PRGVPMPIRGILROLAGHNHRAIMAAFO-----PPPSA 181
QY 215 AVTL-----HIGANGF 225
Db 182 AAVLDLSVBRVHHPRVHGNNHGF 204

RESULT 14

```

HAIR_HUMAN	STANDARD;	PRT; 1189 AA.
ID	043593; Q9NP61;	
DT	15-JUL-1999 (Rel. 38, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Hairless protein.	
GN	HR.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX	NCBI_TaxId=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT ALONC ALA-1022.	
RX	MEDLINE=98111143; PubMed=9445480;	
RA	Almad W., Ul Haque M.F., Brancollini V., Tsou H.C., Ul Haque S.,	
RA	Lam H., Alta V.M., Owen J., Delaiguiere M., Frank J.,	
RA	Cesarihlum-Friedman P.B., Leask A., McGrath J.A., Peacocke M.,	
RA	Almad M., Ott J., Christiano A.M.,	
RT	"Alpecia Universalis associated with a mutation in the human hairless	
RT	gene.";	
RL	Science 279:720-724(1998).	
RL	[2]	
RP	SEQUENCE FROM N.A. (ISOFORM LONG), REVISIONS TO 572 AND 774, AND	
RP	TISSUE SPECIFICITY.	
RC	TISSUE=Peripheral blood leukocytes, and Skin fibroblast;	
RX	MEDLINE=99162400; PubMed=10051399;	
RA	Almad W., Zlotogorski A., Pantelejev A.A., Lam H., Almad M.,	
RA	Ul Haque M.F., Abdallah H.M., Dregan L., Christiano A.M.;	
RT	"Genomic organization of the human hairless gene (HR) and	
RT	identification of a mutation underlying congenital atrichia in an Arab	
RT	paestinian family.";	
RL	Genomics 56:141-148(1999).	
RL	[3]	
RP	SEQUENCE FROM N.A., VARIANT ALONC ASP-1136, TISSUE SPECIFICITY, AND	
RP	ALTERNATIVE SPLICING.	
RC	TISSUE=Brain, Fetal brain, and Peripheral blood leukocytes;	
RX	MEDLINE=98409456; PubMed=9736769;	
RA	Cichon S., Anker M., Vogt I.R., Rohleder H., Putzstuck M., Hillemer A.,	
RA	Farooq S.A., Al-Dhafiri K.S., Almad M., Haque S., Riettschel M.,	
RA	Proping P., Kruse R., Noethen M.M.;	
RT	"Cloning, genomic organization, alternative transcripts and mutational	
RT	analysis of the gene responsible for autosomal recessive universal	
RT	congenital alopecia.";	
RL	Hum. Mol. Genet. 7:1671-1679(1998).	
RN	[4]	
RP	VARIANT APL GLN-620.	
RX	MEDLINE=98431781; PubMed=9758627;	
RA	Almad W., Irvine A.D., Lam H., Buckley C., Bingham E.A.,	
RA	Pantelejev A.A., Almad M., McGrath J.A., Christiano A.M.;	
RT	"A missense mutation in the zinc-finger domain of the human hairless	
RT	gene underlies congenital atrichia in a family of Irish travellers.";	
RL	Am. J. Hum. Genet. 63:984-991(1998).	
CC	-1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO	
CC	REGULATE ONE OF THE PHASES OF HAIR GROWTH.	
CC	-1- SUBCELLULAR LOCATION: Nuclear.	
CC	-1- ALTERNATIVE PRODUCTS:	
CC	Event-Alternative splicing; Named isoforms=2;	
CC	Comment=Additional isoforms seem to exist;	
CC	Name=Long;	
CC	IsoId=O43593-1; Sequence=Displayed;	
CC	Name=Short;	
CC	IsoId=O43593-2; Sequence=VSP 004276;	
CC	-1- TISSUE SPECIFICITY: Strongest expression of both isoforms is seen	
CC	in the small intestine, weaker expression in brain and colon, and	
CC	trace expression is found in liver, pancreas, spleen, thymus,	
CC	stomach, salivary gland, appendix and trachea. Long isoform is	
CC	always the most abundant. Long isoform is exclusively expressed at	
CC	low levels in kidney and testis and short isoform exclusively at	
CC	high levels in the skin.	
CC	-1- DISEASE: DEFECTS IN HR ARE THE CAUSE OF ALOPECIA UNIVERSALIS	
CC	(ALONC); A RARE AUTOSOMAL RECESSIVE FORM OF HAIR LOSS. IT IS	
CC	CHARACTERIZED BY HAIR FOLLICLES WITHOUT HAIR.	

CC -1- DISEASE: DEFECTS IN HR ARE THE CAUSE OF ATRICHTIA WITH PAPULAR
 CC LESIONS (APL) (ALSO KNOWN AS CONGENITAL ATRICHTIA). THIS AUTOSOMAL
 CC RECESSIVE DISEASE IS CHARACTERIZED BY PAPILLARY LESIONS OVER MOST
 CC OF THE BODY AND ALMOST COMPLETE ABSENCE OF HAIR.
 CC
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 CC
 CC EMBL AF03196; AAC32258.2; -;
 CC EMBL AJ277249; CAB87577.2; -;
 CC EMBL AJ277250; CAB87577.2; JOINED.
 CC EMBL AJ277251; CAB87577.2; JOINED.
 CC EMBL AJ277252; CAB87577.2; JOINED.
 CC EMBL AJ277253; CAB87577.2; JOINED.
 CC EMBL AJ400825; CAB87577.2; JOINED.
 CC EMBL AJ400826; CAB87577.2; JOINED.
 CC EMBL AJ400827; CAB87577.2; JOINED.
 CC EMBL AJ400828; CAB87577.2; JOINED.
 CC EMBL AJ400829; CAB87577.2; JOINED.
 CC EMBL AJ400830; CAB87577.2; JOINED.
 CC EMBL AJ400831; CAB87577.2; JOINED.
 CC EMBL AJ400832; CAB87577.2; JOINED.
 CC EMBL AJ400833; CAB87577.2; JOINED.
 CC EMBL AJ400834; CAB87577.2; JOINED.
 CC EMBL AJ400835; CAB87577.2; JOINED.
 CC EMBL AJ400836; CAB87577.2; JOINED.
 CC EMBL AJ400837; CAB87577.2; JOINED.
 CC EMBL AJ277165; CAB86602.1; -;
 CC GeneW; HGNC:5172; HR.
 CC MIM; 602302; -;
 CC MIM; 209500; -;
 CC GO; GO:0005634; C:nucleus; NAS.
 CC GO; GO:0003700; P:transcription factor activity; NAS.
 CC GO; GO:0003551; P:regulation of transcription; DNA-dependant; NAS.
 CC InterPro; IPR003347; TF_jmjc.
 CC DR Pfam; PF02373; jmjc; 1.
 CC DR SMART; SM00558; Jmjc; 1.
 CC KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
 CC Metal-binding; Alternative splicing; Disease mutation.
 CC FT ZN-FING 600 625
 CC FT VARSPLIC 1072 1126
 CC FT VARIANT 620 620
 CC FT VARIANT 1022 1022
 CC FT VARIANT 1136 1136
 CC FT CONFLICT 337 337
 CC FT CONFLICT 446 446
 CC FT CONFLICT 584 584
 CC SQ SEQUENCE 1189 AA; 127509 MW; 5E244858716B5DF CRC64;
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 CC Query Match 6.7%; Score 82.5; DB 1; Length 1189;
 CC Best Local Similarity 23.3%; Pred. No. 14;
 CC Matches 71; Conservative 23; Mismatches 92; Indels 119; Gaps 15;
 CC
 CC 3 LRAGDSW--GMLACTCTVLMHLPAVDALNRGTGPGRP-----SI 40
 CC DB LRAGDPLRGLGRLPLPVRPRRLPPGALLMLQEPQCPRRGFLPQEHNRGCGPVLVSGI 877
 CC QY OKTYVDLTRYLHQLRLSLAGTY--LNTLGRP-----ENPPDNRPP----- 77
 CC DB 878 QRTLOCNLTGTEALGALGGVQVALSPGPPQPSLCSITFWGCGSWPELRPKSDESSVLL 937
 CC QY 78 ---RLGAEFLPR-----ATVDEVMRSLNDKRLTL-----QNEYAY----- 110

DB 938 LHRALGDEDTSRVEMTLAASLPLPEYCALHGKLNLSYLPPIGALNRLPRLPQMLAAVGVSPH 997
 QY 111 -SHL-----LCYLRGNLRQAATNLRSLAHFCTSLQSLGSLGAGMALGVLPPPLPET 165
 DB 998 RGHLDATKNLC-----VEVADLVSLVHADTLP----- 1024
 QY 166 EPTWTPGPAHSDFLQKMD--DFWLKEIQTWLMR--SAKDFRLKKKQP--PAAAVTLH 219
 DB 1025 -PAW--HRAQDFLSGLDGBEGMRSQSVSTYWHFRQADQRIRPFLQWCPAGAGLE 1081
 QY 220 LGAHG 224
 DB 1082 PGAPG 1086
 CC
 CC RESULT 15
 CC ID P85B_BOVIN STANDARD; PRT; 724 AA.
 CC AC P23726;
 CC DT 01-NOV-1991 (Rel. 20, Created)
 CC DT 01-NOV-1991 (Rel. 20, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Phosphatidylinositol 3-kinase regulatory beta subunit (PI3-kinase
 CC p85-beta subunit) (Pcdins-3-kinase p85-beta).
 CC GN PIK3R2.
 CC OS Bos taurus (Bovine).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Bovinae; Bos.
 CC OX NCBI_TaxID=9913;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=91191567; PubMed=1707345;
 CC RA Otsu M., Hiles I.D., Goot I., Fry M.J., Ruiz-Larrea F., Panayotou G.,
 CC RA Thompson A., Dhand R., Hsuan J., Totty N., Smith A.D., Morgan S.J.,
 CC RA Courtneidge S.A., Parker P.J., Waterfield M.D.;
 CC RT "Characterization of two 85 kd proteins that associate with receptor
 CC RT tyrosine kinases, middle-T/pp60c-src complexes, and p13-kinase.",
 CC RL Cell 65:91-104(1991).
 CC RN [2]
 CC RP CIRCULAR DICHROISM AND FLUORESCENCE SPECTROSCOPY.
 CC RX MEDLINE=93049176; PubMed=1330535;
 CC RA Panayotou G., Bax B., Gout I., Federwisch M., Wroblewski B., Dhand R.,
 CC RA Fry M.J., Blundell T.L., Wollmer A., Waterfield M.D.;
 CC RT "Interaction of the p85 subunit of PI 3-kinase and its N-terminal SH2
 CC RT domain with a PDGF receptor phosphorylation site: structural features
 CC RT and analysis of conformational changes".
 CC RL EMBO J. 11:4261-4272(1992).
 CC CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE
 CC KINASES, THROUGH ITS SH2 DOMAIN, AND ACTS AS AN ADAPTER, MEDIATING
 CC THE ASSOCIATION OF THE P110 CATALYTIC UNIT TO THE PLASMA MEMBRANE.
 CC CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
 CC SUBUNIT.
 CC CC -1- SIMILARITY: BELONGS TO THE PI3K P85 SUBUNIT FAMILY.
 CC CC -1- SIMILARITY: Contains 1 Rho-GAP domain.
 CC CC -1- SIMILARITY: Contains 2 SH2 domains.
 CC CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC CC
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 CC
 CC EMBL M61746; AAA79510.1; -;
 CC HSSP; P23727; 2PNB.
 CC InterPro; IPR001720; PI3kinase_P85.
 CC InterPro; IPR000198; RhoGAP.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001452; SH3.
 CC Pfam; PF00620; RhoGAP; 1.

DR Pfam; PF00017; SH2; 2.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00678; PI3KINASEP85.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 2.
DR SMART; SM00324; RhOGAP; 1.
DR SMART; SM00352; SH2; 2.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50238; RhOGAP; 1.
DR PROSITE; PS50001; SH2; 2.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain; SH2 domain; Repeat.
FT DOMAIN 4 SH3.
FT DOMAIN 109 291 RHO-GAP.
FT DOMAIN 326 421 SH2 1.
FT DOMAIN 618 712 SH2 2.
SQ SEQUENCE 724 AA; 81059 MW; 9D2BA8B6DB087098 CRC64;

Query Match 6.7%; Score 82; DB 1; Length 724;
Best Local Similarity 21.9%; Pred. No. 8.1;
Matches 66; Conservative 25; Mismatches 71; Indels 140; Gaps 16;

QY 6 GDSWGLAQLCTVLMHLPAVPALN-RTGDPGEGPSIQKTYDLTRYLHQRLSLAGTYLNY 64
DB 42 GVAEGNERCPQSVGW---MPLGINTKRGQDFP-----GTYVEF 77
QY 65 LGP-----PNEPDPNPP-----R 78
DB 78 LGPVALARPPRRPGRPPLPARPRDGPPEPGLTLPDLPQFSPDVAPPILVKLVEAIER 137
QY 79 LGAETL--PRAT-----VDLEWRSINDKRLTONYEAYSHLLCYLRGLNRQAATAEL 129
DB 138 TGLDSYRPPPPAVRTDWSLSDVEQW---DAAALSDVGKF--LIALPAPLVTPPAAAEA 191
QY 130 RSSL-----AHFCTSLQGL--LGSINQ-----VMAALGY----- 156
DB 192 HRALEBAAGPVAPALEPPTLPILHALLTRFLLQHLGKRVAGRAPAPGPAVRALGATFGPLL 251
QY 157 ----PLPQPLPGTEPTWT-PCPAHSDPLQKMDDFWLKELQTLWRSADFNRLKKKQOP 211
DB 252 LRAPPSPSPPGAPDGTETPT--DFPALIVEKLLQEHLE-----EQEVAP 295
QY 212 PA 213
DB 236 PA 297

Search completed: February 9, 2004, 06:15:33
Job time : 13.5 secs

N/Alternate names: growth-promoting activity protein
 C/Species: Gallus gallus (chicken)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
 C/Accession: JH0680; PQ0057
 R/Neuron 8, 1045-1053, 1992
 A/Title: Cloning, expression during development, and evidence for release of a trophic factor
 A/Reference number: JH0680; MUID:92304573; PMID:1610564
 A/Accession: JH0680
 A/Molecule type: mRNA
 A/Residues: 1-195 <LEU>
 A/Cross-References: GB:M80827; NID:G211822; PIDN:AAA48784.1; PID:G211823
 A/Experimental source: eye
 R/Eckenslein, F.P.; Bach, F.; Holbert, T.; Blacher, R.W.; Nishi, R.
 Neuron 4, 623-631, 1990
 A/Title: Purification and characterization of a trophic factor for embryonic peripheral
 A/Reference number: PQ0057; MUID:190211978; PMID:2322465
 A/Accession: PQ0057
 A/Molecule type: protein
 A/Residues: 155-166, 'X', 168-175 <ECK>
 A/Experimental source: sciatic nerves
 C/Comment: This is a neurotrophic protein.
 C/Superfamily: ciliary neurotrophic factor
 C/Keywords: growth factor

Query Match 7.4%; Score 91; DB 2; Length 195;

Best Local Similarity 27.3%; Pred. No. 0.53; Matches 51; Conservative 21; Mismatches 83; Indels 32; Gaps 9;

46 LTRYLEHQRLSLAGTYLNYLPGPPFPNPRGLGAETLPRAVTDLVWRSLNDKRLTQ 105

23 LARKRSVDVTDLIDIVERQ-----LDASISVAADVPTAAV--ERVAEGTGTOGLID 75

106 N---YEAYHLLCYLRGLNRQA---ATAIIRSLA-----HFTCSLGLIGSLAGVNA 152

76 NIAAARAFTLLAQMLEEGRELDGTDALGPALAMLLQVSAFYHLELL-----ELE 130

153 ALGYPLPQLPGTEPTWGPAN--SDFLQKMDFWLTKELTWLRSAKDPFRLKKKQ 211

131 SRGAPAE---GSEP---PAPRLSLFEQKLGKGLVRLKLAQAVRSVADLRQLSKGPG 184

212 PAAAVTL 218

185 SGALGL 191

RESULT 7

138943 Probable guanine nucleotide binding protein - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C/Accession: T38943
 R/Skelton, J.; Churcher, C.M.; Barrett, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, May 1997
 A/Reference number: Z21819

A/Accession: T38943
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-113 <SKE>

A/Cross-References: EMBL:Z95396; PIDN:CA08769.1; GSPDB:GN00066; SPDB:SPAC57A7.11

A/Experimental source: strain 97zh-; comid c57A7
 C/Genetics:

A/Gene: SPDB:SPAC57A7.11
 A/Map position: 1

Query Match 7.3%; Score 89.5; DB 2; Length 113;

Best Local Similarity 22.8%; Pred. No. 8; Matches 61; Conservative 32; Mismatches 69; Indels 105; Gaps 14;

15 LCTVLMHLPAV--PALNR-----TGDPGPGPSI-----OKTYDLTRYLEHQRLS 56

811 LAFLLQHLPAHLKASISKDTDTNVTSDPKPPFVPSVSENKLNRSELTSLKGLALS 870

57 LAG-----TYLNYL-----GPP-FNEPDFNPRLGAETLPRAVTDL 91

871 LAGSRASELSINGENKPAESNNHLTSAVCPGPAANELEY-----QSEIDM 919

92 EWRMSLND-----KLRLTONYEAYSHLLCYLRGL--NRQATVLELRSLAHFCTS 139

920 PLTSLYLFWSKRYFTPEQMRNEDEDPSS--ICYNQRLMRNRNREKLYRTPLAEVSTN 977

140 -----LQGLLSIAGVAAALGYPLPQLPCTEPTWGPANSDFLQKMDFWLKE--- 190

978 GRNQQLTFNNNTIA-----PRKLMHPQEDQLITLGDKDI 1013

191 LQVWDMR-----NRCNLSFKTSASATT 1036

978 GRNQQLTFNNNTIA-----PRKLMHPQEDQLITLGDKDI 1013

191 LQVWDMR-----NRCNLSFKTSASATT 1036

978 GRNQQLTFNNNTIA-----PRKLMHPQEDQLITLGDKDI 1013

191 LQVWDMR-----NRCNLSFKTSASATT 1036

978 GRNQQLTFNNNTIA-----PRKLMHPQEDQLITLGDKDI 1013

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191 LQVWDMR-----NRCNLSFKTSASATT 1036

978 GRNQQLTFNNNTIA-----PRKLMHPQEDQLITLGDKDI 1013

191 LQVWDMR-----NRCNLSFKTSASATT 1036

978 GRNQQLTFNNNTIA-----PRKLMHPQEDQLITLGDKDI 1013

191 LQVWDMR-----NRCNLSFKTSASATT 1036

A:Residues: 1-955 <MAT>
 A:Cross-references: EMBL:AB012266; NID:d1227741; PIDN:BAA32791.1; PID:d1033757
 A:Experimental source: brain
 C:Genetics:
 A:Gene: w1z

Query Match 7.1%; Score 87; DB 2; Length 955;
 Best Local Similarity 27.8%; Pred. No. 9.1;
 Matches 35; Conservative 19; Mismatches 48; Indels 24; Gaps 7;

QY 22 LPVAVLNRTGDPGPGPSIQKTYDITRYLEHQLRSLAG--TYLNTYLG---PENEED 73
 DB 615 LPLSLPASRPGRKPGAGPT-----QVPR--ELSLSPITGSKPSAASYLGAVATKRPLQEDR 667
 QY 74 FNPRLGAEPLPRATVDLEWRSINDKRLTQNYEAVSHLCTYLRGL--NRQATAEIR 130
 DB 668 FLPAEVKATYIQTLELPPKA-KTLHEK-----TSHSTACEGCLGYFENRKALASHAR 721
 QY 131 RSLAHF 136
 DB 722 AHLRQF 727

RESULT 10

T00248
 zinc finger protein w1zL - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
 R:Accession: T00248
 R:Matsumoto, K.; Ishii, N.; Yoshida, S.; Shiosaka, S.; Wanaka, A.; Tohyama, M.
 A:Submitted to the EMBL Data Library, March 1998
 A:Description: Molecular cloning and distinct developmental expression pattern of splice
 A:Reference number: Z14130
 A:Accession: T00248
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1561 <MAT>
 A:Cross-references: EMBL:AB012265; NID:d1227740; PIDN:BAA32790.1; PID:d1033756
 A:Experimental source: brain
 C:Genetics:
 A:Gene: w1z

Query Match 7.1%; Score 87; DB 2; Length 1561;
 Best Local Similarity 27.8%; Pred. No. 17;
 Matches 35; Conservative 19; Mismatches 48; Indels 24; Gaps 7;

QY 22 LPVAVLNRTGDPGPGPSIQKTYDITRYLEHQLRSLAG--TYLNTYLG---PENEED 73
 DB 1221 LPLSLPASRPGRKPGAGPT-----QVPR--ELSLSPITGSKPSAASYLGAVATKRPLQEDR 1273
 QY 74 FNPRLGAEPLPRATVDLEWRSINDKRLTQNYEAVSHLCTYLRGL--NRQATAEIR 130
 DB 1274 FLPAEVKATYIQTLELPPKA-KTLHEK-----TSHSTACEGCLGYFENRKALASHAR 1327
 QY 131 RSLAHF 136
 DB 1328 AHLRQF 1333

RESULT 11

T34916
 transferase - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Sep-2000
 R:Accession: T34916
 R:Olliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 A:Submitted to the EMBL Data Library, January 1998
 A:Reference number: Z21558
 A:Accession: T34916
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-640 <OLIS>
 A:Cross-references: EMBL:AL021409; PIDN:CAI16181.1; GSPDB:GN00070; SCOEDB:SC3F7.10

A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCORDB:SC3F7.10
 C:Superfamily: glycine C-acetyltransferase homology
 F:287-624/Domain: glycine C-acetyltransferase homology <GCA>

Query Match 7.1%; Score 86.5; DB 2; Length 640;
 Best Local Similarity 27.2%; Pred. No. 6.1;
 Matches 50; Conservative 13; Mismatches 64; Indels 57; Gaps 9;

QY 22 LPVAVLNRTGDPGPGPSIQKTYDITRYLEHQL--RSLAGTYLNTYLGPPNEEDFNPBR 78
 DB 100 LPVAVPA-EGTGDPVTEAVVAAMRQYQRHQLGIDADLEG-----E 140
 QY 79 LGAETLPRAATVDLEWRSINDKRLTQNYEAVSHLCTYLRGLNRQATAEIRSLAHFCT 138
 DB 141 LGVDSVVLTSVAEE--TERLGLT-----GAAPDAAGATTTLALA---D 179
 QY 139 SLQGLGSIAGVMAALGYPLPQPLGTEPTWTPGPAHSDFLOKMDFWLKLQETWLR 198
 DB 180 ALRGL-----VAAAPGTAIVEAAPTGA-AAPAGRGGNP-----ARGADGMDHRS 225
 QY 199 AKDF 202
 DB 226 MKDF 229

RESULT 12

C38604
 poly(3-hydroxyalkanoate) polymerase (EC 2.7.7.-) 3 - Pseudomonas oleovorans
 C:Species: Pseudomonas oleovorans
 C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Sep-2000
 R:Accession: C38604
 R:Huisman, G.W.; Konink, B.; Meima, R.; Kazemier, B.; Terpstra, P.; Witholt, B.
 J. Biol. Chem. 266, 2191-2198, 1991
 A:Title: Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas oleovorans. Ident
 A:Reference number: A38604; MUID:91115830; PMID:1989978
 A:Accession: C38604
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-560 <HUI>
 A:Cross-references: GB:M58445; NID:G151441; PIDN:AAA25934.1; PID:G151444
 C:Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
 C:Keywords: nucleotidyltransferase

Query Match 7.0%; Score 85.5; DB 2; Length 560;
 Best Local Similarity 30.2%; Pred. No. 6.4;
 Matches 38; Conservative 17; Mismatches 42; Indels 29; Gaps 7;

QY 77 PRIGAEPLPRATVDLEWRSINDKRLTQNYEAVSHLCTYLRGLNRQATAEIRSL--A 134
 DB 5 PAKGPTLPATSMNVQ-----NALIGLRG-----DLSTLRNVSROS-----LRHPLHTA 50
 QY 135 HECTSLQGLGSIAGVMAALGYPLPQPLG--TEPTWTPGPAHSDFLOKMDFWLKE 190
 DB 51 HHLALGGQLGRV-----ILGDTPLQPNRPDRSDPTWSONPFYRRLGQ---YLAWQ 101
 QY 191 LQTLWM 196
 DB 102 KQTRLW 107

RESULT 13

F72511
 probable cystathionine gamma-synthase APE2068 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 R:Accession: F72511
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takat
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, U.; K
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: F72511
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-389 <KAW>
 A:Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BAA81078.1; PID:95105766
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: ABE2068
 C:Superfamily: O-succinylhomoserine (thiol)-lyase

Query Match 6.9%; Score 84.5; DB 2; Length 389;
 Best Local Similarity 22.9%; Pred. No. 5;
 Matches 47; Conservative 19; Mismatches 78; Indels 61; Gaps 8;

QY 43 TYDLRYLEHQLSLAGTLYLVLPFNPDPFPRPLGAEFLPRATVDLEWRSL----- 97
 DB 107 TFGSTRSLLEMLSSITGIEVRLAGPWE-----LLDVLVCAADLIVES 150
 QY 98 --NDKLRLTONYEAVSHLLCYLGLNRQATAELR-----RSL--AHFCTS 139
 DB 151 MANPLTRVPP-----LSGIYREAGSGVRVVTATPTATPLRGAAHY--S 197
 QY 140 LQGLGSIAGVMAALGYPLPQPL-PGTEPTWTPGPAHSDFLQKMDFFLLKSLQTWLWS 198
 DB 198 LBSLTGYIAGNDVVGSLSGRVEEDLEPLMMRKILGTIMQPIDAY-----LAWRG 249
 QY 199 AKDFNRLLKKKQPPAAAVTLHLGAH 223
 DB 250 MKTLKARFEAGRAAVEVAEMLESH 274

RESULT 14

AD3633
 Hypothetical protein BMEI10989 [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C:Accession: AD3633
 R:DelVecchio, V.G.; Kaparatel, V.; Redkar, R.J.; Patra, G.; Muir, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltzman, E.; Selkov, E.; Elser, P.H.; Haglue, S.; O'Callaghan, D.; Letese Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AD3633
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-200 <KUR>
 A:Cross-references: GB:AE008918; PIDN:AAL54231.1; PID:917985203; GSPDB:GN00191
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI10989
 A:Map position: 11

Query Match 6.9%; Score 84; DB 2; Length 200;
 Best Local Similarity 24.3%; Pred. No. 2.4;
 Matches 56; Conservative 22; Mismatches 84; Indels 68; Gaps 13;

QY 10 GMLACCTVLMHLPAVPALNRGDPGPGSIQKTYDLYLHQLSLAGTLYLVLP 69
 DB 2 GLAGALV--LPSPAPAKTQQAAMPNATSPHQADVYL--LRGFADIFSTGI---- 51
 QY 70 NEPDFNPRLGAEFLPRATVDLEV-----WRSINDKLRLTONYEAVSHLLCYLRG--LNR 122
 DB 52 -----DEIGAE-LQAAGVNAHVQGAAMRLVYN--RIVADQKXGHLPLVILIGSLGA 101
 QY 123 QAA--TAELRSLAHFCTSLQGLSAGVMAALGYPLPQPLPGT-----EPTW 169
 DB 102 NNAIYIAEELER-----RGIAVDYMATFAATG---PDLPGNVRVVPFYFKQHG 149
 QY 170 ----TGPCPAHSDFLQKMDFFLLKSLQTWLMSAKDFNRLLKKKQPPAA 215
 DB 150 GLPLVGPSPRPHGLENR-----FSNAKOVGHFNIEKORPLQA 187

RESULT 15

F75439
 Probable cell wall synthesis protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: F75439
 R:White, O.; Eileen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Me S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: F75439
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-411 <WHI>
 A:Cross-references: GB:AE001958; GB:AE000513; NID:96458805; PIDN:AAF10649.1; PID:9645880
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1076
 A:Map position: 1

Query Match 6.9%; Score 84; DB 2; Length 411;
 Best Local Similarity 24.6%; Pred. No. 6;
 Matches 56; Conservative 25; Mismatches 77; Indels 70; Gaps 11;

QY 2 DLRADSGMGLACCTVLMHLPAVPALNRGDPGPGSIQKTYDLYLHQLSLAGT 61
 DB 212 EYLAADRVALRAELPSEMSLRGVPDLLLSGG-GRGHVAAAADVLT-----ELGNL-GR 264
 QY 62 LNYLGPFPNPDPFNPRLGAEFLPRATVDLEWRSLNDKLRLTONYEAVSHLLCYLRGIN 121
 DB 265 VQVLVPARQGE-----GTETIGATV-----HHLGFRRLD 296
 QY 122 RQAAVLAELRSLAHFCTSLQGLSAGV---MAALGYPLP--QPLPGTEPTWTPGPAH 175
 DB 297 RLAAASDL-----VVGKAGGLTVAEATALGVPVLYVAPIPQGE-----EHN 337
 QY 176 SPFLQKMDFFLLKSLQTWLW-MSAKDFNRLLKKKQPPAAAVTLHLGA 222
 DB 338 ADFLERHG-----AGLWARRAHVDVPLVLRALDPAEHARLSAGA 376

Search completed: February 9, 2004, 06:17:41
 Job time : 21 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using BW model

Run on: February 9, 2004, 06:10:24 ; Search time 349.674 Seconds
(without alignments)
8395.981 Million cell updates/sec

Title: US-09-931-704-1

Perfect score: 797
Sequence: 1 attaaagcttcgacgagcc.....ctctccttcgctccccc 797

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: Published Applications NA.*
 - 2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUBCOMB.seq.*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUBCOMB.seq.*
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 - 11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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 - 14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
 - 15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
 - 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 17: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
 - 18: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	9	US-09-931-704-1
2	749.4	94.0	1710	15	US-10-212-793-1
3	669.4	84.0	819	9	US-09-931-704-4
4	523.4	65.7	5087	9	US-09-931-704-3
5	493.4	61.9	495	9	US-09-864-761-23175
6	369	46.3	492	9	US-09-864-761-6462
7	269.4	33.8	283	10	US-09-765-231A-75
8	175.8	22.1	809	13	US-10-027-632-134702
9	175.8	22.1	396	15	US-10-027-632-134702
10	80.2	10.1	396	15	US-10-212-793-7
11	58.6	5.9	65	13	US-09-908-975-29446
12	46.8	5.6	2320	15	US-10-102-806-266
13	44.8	5.6	68750	14	US-10-014-717-1
14	43.6	5.5	3195	12	US-10-295-027-1127
15	43.6	5.5	3195	13	US-10-285-976-54

16	43.6	5.5	3195	15	US-10-205-823-143	Sequence 143, App
17	41.8	5.2	594	13	US-10-140-472-10	Sequence 10, Appl
18	41.8	5.2	594	13	US-10-141-761-10	Sequence 10, Appl
19	41.8	5.2	594	13	US-10-142-885-10	Sequence 10, Appl
20	41.8	5.2	594	13	US-10-142-885-10	Sequence 10, Appl
21	41.8	5.2	594	13	US-10-158-790-10	Sequence 10, Appl
22	41.8	5.2	594	13	US-10-140-805-10	Sequence 10, Appl
23	41.8	5.2	594	13	US-10-140-805-10	Sequence 10, Appl
24	41.8	5.2	594	13	US-10-140-864-10	Sequence 10, Appl
25	41.8	5.2	594	13	US-10-140-923-10	Sequence 10, Appl
26	41.8	5.2	594	13	US-10-141-756-10	Sequence 10, Appl
27	41.8	5.2	594	13	US-10-141-759-10	Sequence 10, Appl
28	41.8	5.2	594	15	US-10-123-155-10	Sequence 10, Appl
29	41.8	5.2	594	16	US-10-146-731-10	Sequence 10, Appl
30	40.8	5.1	1581	12	US-10-369-493-13081	Sequence 43081, A
31	40.4	5.1	1083	15	US-10-156-761-2132	Sequence 176, App
32	40.4	5.1	9025608	15	US-10-156-761-1	Sequence 3132, App
33	40.2	5.0	586	15	US-10-008-063-1	Sequence 1, Appl1
34	40.2	5.0	586	15	US-10-152-363A-59	Sequence 59, Appl
35	39.8	5.0	653	15	US-10-184-644-402	Sequence 402, App
36	39.8	5.0	653	15	US-10-184-634-402	Sequence 402, App
37	39.8	5.0	2247	15	US-10-156-761-7471	Sequence 7471, App
38	39.8	5.0	4641	12	US-10-369-493-24230	Sequence 24230, A
39	39.2	4.9	786	13	US-10-259-165-705	Sequence 705, App
40	39.2	4.9	5452	12	US-10-292-798-1189	Sequence 1189, App
41	39.2	4.9	5452	13	US-10-017-161-1481	Sequence 1481, App
42	39.2	4.9	9025608	15	US-10-156-761-1	Sequence 1, Appl1
43	39	4.9	440	13	US-10-063-605-52	Sequence 52, Appl
44	39	4.9	440	15	US-10-184-644-202	Sequence 202, App
45	39	4.9	440	15	US-10-184-634-202	Sequence 202, App

ALIGNMENTS

RESULT 1
US-09-931-704-1
Sequence 1, Application US/09931704
Patent No. US20020041873A1
GENERAL INFORMATION:
APPLICANT: Senaldi, Giorgio
TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using N
FILE REFERENCE: A-695
CURRENT APPLICATION NUMBER: US/09/931,704
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/226,436
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (90)..(764)
OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: (171)..()
OTHER INFORMATION: Met at -27
US-09-931-704-1
Query Match 100.0%; Score 797; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.2e-204;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATTAAGCTTGGCCGAGACCGGCTCCCTCCACTCCGCGACCTCCCGGAGAGAG 60
DB 1 ATTAAGCTTGGCCGAGACCGGCTCCCTCCACTCCGCGACCTCCCGGAGAGAG 60
QY 61 CCGACCCGCGCGCCGAGCCGACGACCTCCGAGAGAGAGAGAGAGAGAGAGAG 120

Db	61	CCGACCCGGCCGGCCAGCCTCCAGCCCATGGACCTCCGAGGAGGGGAACTGTGGGGGA	120
OY	121	TGTTAGCGTGCCTGTGTCAGAGGTGCTGTGGCACTCCCTGAGTGGCCAGCTCTCAATGCA	180
Db	121	TGTTAGCGTGCCTGTGTCAGAGGTGCTGTGGCACTCCCTGAGTGGCCAGCTCTCAATGCA	180
OY	181	CAGGGGAACTCAGGGGCTGGGCCCCCTCCATCCAGAAACCTATGACTCACCCTGACTGTG	240
Db	181	CAGGGGAACTCAGGGGCTGGGCCCCCTCCATCCAGAAACCTATGACTCACCCTGACTGTG	240
OY	241	AGCACCAACTCCGACAGCTTGGCTGGGACCTATCTGAATCACTCGGGGCCCCCTTTCAAG	300
Db	241	AGCACCAACTCCGACAGCTTGGCTGGGACCTATCTGAATCACTCGGGGCCCCCTTTCAAG	300
OY	301	AGCCAGACTTCAACCTCTCCCGCTGTGGGGGACAGACTCTGCCAGGGCCACTGTGACT	360
Db	301	AGCCAGACTTCAACCTCTCCCGCTGTGGGGGACAGACTCTGCCAGGGCCACTGTGACT	360
OY	361	TGGAGGTGGGGGAAGCCTCATATGACAAACTCGGGCTGACCCAGAACTTACGAGGCTTAC	420
Db	361	TGGAGGTGGGGGAAGCCTCATATGACAAACTCGGGCTGACCCAGAACTTACGAGGCTTAC	420
OY	421	GCCACCTTCTGTGTTACTTGGCTGGGCTCAACCGTACAGCTGGCACTGTGAGCTGCGC	480
Db	421	GCCACCTTCTGTGTTACTTGGCTGGGCTCAACCGTACAGCTGGCACTGTGAGCTGCGC	480
OY	481	GCAGCTTGAGCCACTTCTTGACACAGCCTTCAGGGCTGCTGGGGACAGATTGGGGGCTCA	540
Db	481	GCAGCTTGAGCCACTTCTTGACACAGCCTTCAGGGCTGCTGGGGACAGATTGGGGGCTCA	540
OY	541	TGGCAGCTCTGGGCTAACCCACTGCCCCACCGCTGCTGGGACTGAACCCACTTGGACTC	600
Db	541	TGGCAGCTCTGGGCTAACCCACTGCCCCACCGCTGCTGGGACTGAACCCACTTGGACTC	600
OY	601	CTGGGCTTGCCCCACAGTGACTTCTCTCAGAAGTGGAGCACTTTCGGCTGCTGGAAGAGC	660
Db	601	CTGGGCTTGCCCCACAGTGACTTCTCTCAGAAGTGGAGCACTTTCGGCTGCTGGAAGAGC	660
OY	661	TGCAGACCTGAGCTGTGGGCTTCGGGCCAAGACTTCAACCGGCTCAAGAAGAAATGCACG	720
Db	661	TGCAGACCTGAGCTGTGGGCTTCGGGCCAAGACTTCAACCGGCTCAAGAAGAAATGCACG	720
OY	721	CTCCAGCAGCTGCACTGCACTCTGCACTGGGGGCTCATGGCTTCTGACCTTCT	780
Db	721	CTCCAGCAGCTGCACTGCACTCTGCACTGGGGGCTCATGGCTTCTGACCTTCT	780
OY	781	CCTCTTGGCTCCCCCC 797	
Db	781	CCTCTTGGCTCCCCCC 797	

```

1 RESULT 2 US-10-212-793-1.
2
3 ? Sequence 1, Application US/10212793
4 ? Publication No. US20030087395A1
5 ? GENERAL INFORMATION:
6 ? APPLICANT: Shi et al.
7 ? TITLE OF INVENTION: Cardiotoxin-like Cytokine
8 ? FILE REFERENCE: P34851C1
9 ? CURRENT APPLICATION NUMBER: US/10/212,793
10 ? CURRENT FILING DATE: 2002-08-07
11 ? PRIOR APPLICATION NUMBER: US 09/438,299
12 ? PRIOR FILING DATE: 1999-11-12
13 ? PRIOR APPLICATION NUMBER: US 09/106,182
14 ? PRIOR FILING DATE: 1998-06-29
15 ? PRIOR APPLICATION NUMBER: US 60/051,311
16 ? PRIOR FILING DATE: 1997-06-30
17 ? NUMBER OF SEQ ID NOS: 24
18 ? SEQ ID NO 1
19 ? LENGTH: 1710
20 ? TYPE: DNA
21 ? ORGANISM: homo sapiens
22 ? FEATURE:
23

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; LOCATION: CDS
; OTHER INFORMATION: (46)..(720)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (46)..(126)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (127)..(720)
US-10-212-793-1

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Query Match	94.0%;	Score 749.4;	DB 15;	Length 1710;
Best Local Similarity	99.9%;	Pred. No. 2.6e-191;		
Matches 750; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Oy	45	GCTCTGGGAGAGAGAACCGCACCCGGGCGGCGCAGACCCAGCCTCCATGAGACTCCAGCA	104
Dp	1	GCTTCCGGGAGAGAGACCCGACCCGGCGGCGCGCCAGCCTCCAGACTCCAGCA	60
Oy	105	GGGGACTCGTGGGGGATGTTAAGCTGCTGTGACAGGAGTCTTGAGCACTCCCTGCAGTG	164
Dp	61	GGGGACTCGTGGGGGATGTTAAGCTGCTGTGACAGGAGTCTTGAGCACTCCCTGCAGTG	120
Oy	165	CCAGCTCTCAATCGCACAGGGGACCCAGGGCTTGCGCCCTTCATCCAGAAACTCATGAC	224
Dp	121	CCAGCTCTCAATCGCACAGGGGACCCAGGGCTTGCGCCCTTCATCCAGAAACTCATGAC	180
Oy	225	CTACCCGCTACCTGAGAGCAACCACTCGCAGCTTGGCTGGGACCTATGAACTACCTG	284
Dp	181	CTACCCGCTACCTGAGAGCAACCACTCGCAGCTTGGCTGGGACCTATGAACTACCTG	240
Oy	285	GGCCCCCTTTCAGAGAGCAGACTTCAACCTCCCGCCTGGGGGACAGACTTGGCC	344
Dp	241	GGCCCCCTTTCAGAGAGCAGACTTCAACCTCCCGCCTGGGGGACAGACTTGGCC	300
Oy	345	AGGGCCACTGTTGACTTGGAGGTGTGGGAGCCTCAATGACAAACTGCGGCTGACCCAG	404
Dp	301	AGGGCCACTGTTGACTTGGAGGTGTGGGAGCCTCAATGACAAACTGCGGCTGACCCAG	360
Oy	405	AACTAGAGAGCCTACAGACCACTCTGTACTTGGTGGGCCCAACGTCAGGCTGCC	464
Dp	361	AACTAGAGAGCCTACAGACCACTCTGTACTTGGTGGGCCCTCAACCGTCAGGCTGCC	420
Oy	465	ACTGCTGAGCTGCGCGGAGCCTGGCCACTTCTGACACAGACCTCCAGGGCCTGCTGGGC	524
Dp	421	ACTGCTGAGCTGCGCGGAGCCTGGCCACTTCTGACACAGCTCCAGGGCCTGCTGGGC	480
Oy	525	AGCATTCGAGGCGTATGAGCACTTGGGCTTACCCACTGCCCCAGCGCTGCTGGAGCT	584
Dp	481	AGCATTCGAGGCGTATGAGCACTTGGGCTTACCCACTGCCCCAGCGCTGCTGGAGCT	540
Oy	585	GAACCCACTTGAACCTCGGCGCTGGCCACAGTACACTTCTCCAGAAAGATGAGACACTTC	644
Dp	541	GAACCCACTTGAACCTCGGCGCTGGCCACAGTACACTTCTCCAGAAAGATGAGACACTTC	600
Oy	645	TGAGCTGCTAAGAGAGCTGACAGACTTGAGGTGGGAGCTTGCGCAAGAGACTTCAACCGAGCTC	704
Dp	601	TGAGCTGCTAAGAGAGCTGACAGACTTGAGGTGGGAGCTTGCGCAAGAGACTTCAACCGAGCTC	660
Oy	705	AAGAGAGAGATGACAGCTTCAGCAGCTGACATCACTCGAGACCTGGGGGCTCATGGCTTC	764
Dp	661	AAGAGAGAGATGACAGCTTCAGCAGCTGACATCACTCGAGACCTGGGGGCTCATGGCTTC	720
Oy	765	TGACTTCTGACTTCTCTCTCTTGGCTCCCC	795
Dp	721	TGACTTCTGACTTCTCTCTCTTGGCTCCCC	751

RESULT 3
US-09-931-704-4
; Sequence 4, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio

TITLE OF INVENTION: Methode and Compositions for Treating Ige-Related Disease Using N
FILE OF INVENTION: Inhibitors
FILE REFERENCE: A-695
CURRENT APPLICATION NUMBER: US/09/931,704
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/226,436
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 819
TYPE: DNA
ORGANISM: Murine
FEATURE:
NAME/KEY: CDS
LOCATION: (95)..(769)
OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: (176)..()
OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: (176)..(769)
OTHER INFORMATION:
NAME/KEY: 819_peptide
LOCATION: (95)..(175)
OTHER INFORMATION:
US-09-931-704-4

Query Match 84.0%; Score 669.4; DB 9; Length 819;
Best Local Similarity 92.0%; Pred. No. 7.1e-170;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

1 ATTAAGCTTCCCGGAGCGCGGCTCGCCCTCCCACTCCGACGCTCCGGAGAGAG 60
5 ATTAAGCTTCCCGGAGCGCGGCTCGCCCTCCCACTCCGACGCTCCGGAGAGAG 64
61 CCGACCCGCGGCGCGGAGCGCGGCTCGCCCTCCCACTCCGACGCTCCGGAGAG 119
65 CCGCGCGCGCGCGGCGCGGCTCGCCCTCCCACTCCGACGCTCCGGAGAGAG 124
120 ATGTTAGCGTGCCTGTCACGGTGTCTGTGGACCTTCCTGCACTGCTCAATCC 179
125 ATGTTAGCTTGGCTATGACAGGTTGTGTGGACCTTCCTGCACTGCTCAATCC 184
180 AAGAGGAGACCGAGGCGCGGCTCGCCCTCCCACTCCGACGCTCCGGAGAGAG 239
185 AAGAGGAGATCCAGGCGCGGCTCGCCCTCCCACTCCGACGCTTCACCGCTAC 244
240 GAGACCAACTCCGAGCTTGGCTGGAGCTTATCTGAACTACCTGGGCGCGCTTCA 299
245 GAGACCAACTCCGAGCTTGGCTGGAGCTTATCTGAACTACCTGGGCGCGCTTCA 304
300 GAGCGAGACTTCAACCTCCCGGCTGGGCGGAGAGACTCTGCCAGGCGCACTGTG 359
305 GAGCGAGACTTCAACCTCCCGGCTGGGCGGAGAGACTCTGCCAGGCGCACTGTG 364
360 TTGAGAGTGTGGAGAGCTCAATGACAACTGGCGGCTGACCCAGAACTATGAG 419
365 TTGAGAGTGTGGAGAGCTCAATGACAACTGGCGGCTGACCCAGAACTATGAG 424
420 AGCGACCTTCTGTGTTACTTGGTGGGCTCAACCGTCAAGGCTGACCTGAGCTG 479
425 AGTCACTTCTGTGTTACTTGGTGGGCTCAACCGTCAAGGCTGACCTGAGCTG 484
480 CGCAGCGTGGCCCACTTCTGACCAAGCTTCAGGCGCTGCTGGGAGAGCTTGG 539
485 CGTACGCTGGCCCACTTCTGACCAAGCTTCAGGCGCTGCTGGGAGAGCTTGG 544
540 ATGAGAGCTTCTGGGCTACCACTGCGCGGCTGCTGGGAGAGCTTGGAGCT 599
545 ATGAGAGCTTCTGGGCTACCACTGCGCGGCTGCTGGGAGAGCTTGGAGCT 604
600 CTTGGCGCTGCCCAAGTGAAGTATGAGAGTGAAGTGAAGTGAAGTGAAGTGA 659

605 CTTGGCGCTGCCCAAGTGAAGTATGAGAGTGAAGTGAAGTGAAGTGAAGTGA 664
660 CTTGGCGCTGCCCAAGTGAAGTATGAGAGTGAAGTGAAGTGAAGTGAAGTGA 719
665 CTTGGCGCTGCCCAAGTGAAGTATGAGAGTGAAGTGAAGTGAAGTGAAGTGA 724
720 CTTGGCGCTGCCCAAGTGAAGTATGAGAGTGAAGTGAAGTGAAGTGAAGTGA 778
725 CTTGGCGCTGCCCAAGTGAAGTATGAGAGTGAAGTGAAGTGAAGTGAAGTGA 783

RESULT 4
US-09-931-704-3
Sequence 3, Application US/09931704
Patent No. US20020041873A1

GENERAL INFORMATION:
APPLICANT: Senaldi, Giorgio
TITLE OF INVENTION: Methode and Compositions for Treating Ige-Related Disease Using
FILE OF INVENTION: Inhibitors

CURRENT APPLICATION NUMBER: US/09/931,704
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/226,436
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 5087
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (137)..(138)
OTHER INFORMATION: product = "INTERVENING UNSEQUENCED REGION OF >1KB"

US-09-931-704-3
Query Match 65.7%; Score 523.4; DB 9; Length 5087;
Best Local Similarity 99.8%; Pred. No. 1.1e-130;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

271 ATCTGAATCTAGTGGGCGCGGCTTTCAGAGAGAGAGAGAGAGAGAGAGAG 330
3363 AGCTGAATCTAGTGGGCGCGGCTTTCAGAGAGAGAGAGAGAGAGAGAGAG 3422
331 CAGAGACTCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390
3423 CAGAGACTCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3482
391 TGGCGCTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
3483 TGGCGCTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3542
451 ACCGTGAG 510
3543 ACCGTGAG 3602
511 AGGCGCTGAG 570
3603 AGGCGCTGAG 3662
571 CGTGGCTGAG 630
3663 CGTGGCTGAG 3722
631 AGATGAG 690
3723 AGATGAG 3782
691 ACTTGAACCGGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
3783 ACTTGAACCGGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3842

QY 751 GGGCTCATGCTTGTGACTTGTGACCTTCTCTTGGCTCCCC 795
DB 3843 GGGCTCATGCTTGTGACTTGTGACCTTCTCTTGGCTCCCC 3887
US-09-864-761-23175/c
; Sequence 23175, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23175
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005649.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: SWISSPROT HIT: Q63086, EVALU8 8.00e-03
; OTHER INFORMATION: NT HIT: g11439486, EVALU8 0.00e+00

; OTHER INFORMATION: EST_HUMAN HIT: A1752561.1, EVALU8 0.00e+00
US-09-864-761-23175
Query Match 61.9%; Score 493.4; DB 9; Length 495;
Best Local Similarity 99.8%; Pred. No. 1.1e-122;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 273 CTGAACCTAGTGGGCCCCCTTTCACAGAGCAGACTTCAACCCCTCCGCTGGGGGCA 332
DB 495 CTGAACCTAGTGGGCCCCCTTTCACAGAGCAGACTTCAACCCCTCCGCTGGGGGCA 436
QY 333 GAGACTTGGCCAGGGCCACTGTGACTTGGAGGTGTGGCAAGCTCAATGACAACTG 392
DB 435 AAGACTTGGCCAGGGCCACTGTGACTTGGAGGTGTGGCAAGCTCAATGACAACTG 376
QY 353 CGGCTGACCCAGAACTAGAGAGCCCTACAGCCCACTTGTGTACTTGGCGGCTCAAC 452
DB 375 CGGCTGACCCAGAACTAGAGAGCCCTACAGCCCACTTGTGTACTTGGCGGCTCAAC 316
QY 453 CGTCAGGCTGCACTGTGACTGAGCGGCGCAGCCCTGCGCCACTTGTGACAGCCTCCAG 512
DB 315 CGTCAGGCTGCACTGTGACTGAGCGGCGCAGCCCTGCGCCACTTGTGACAGCCTCCAG 256
QY 513 GGCCTGCTGGGCGAGCATTTGGGGCGTCATGGCACTTGGGCTACCACTGCCCCAGCG 572
DB 255 GGCCTGCTGGGCGAGCATTTGGGGCGTCATGGCACTTGGGCTACCACTGCCCCAGCG 196
QY 573 CTGCTGAGGACTGAACCACTTGAATCTTGGCCCTGCGCCACATGACTTCTCCAGAG 632
DB 195 CTGCTGAGGACTGAACCACTTGAATCTTGGCCCTGCGCCACATGACTTCTCCAGAG 136
QY 633 ATGACGACTTCTGAGCTGTAAGAGAGCTGAGAGCTGTGAGCGCTGCGCCAGAGAC 692
DB 135 ATGACGACTTCTGAGCTGTAAGAGAGCTGAGAGCTGTGAGCGCTGCGCCAGAGAC 76
QY 753 TTCAACCGGCTCAAGAGAGATGAGCTTCACAGAGCTGAGTACCTTGCACCTGGGG 752
DB 75 TTCAACCGGCTCAAGAGAGATGAGCTTCACAGAGCTGAGTACCTTGCACCTGGGG 16
QY 753 GCTCATGCTTCTGA 767
DB 15 GCTCATGCTTCTGA 1
RESULT 6
; Sequence 6462, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

Query Match	Similarity	Score	DB	Length
Best Local	Similarity	100.0%	Pred. No.	2,56-89
Matches	369	Conservative	0	Mismatches
			0	Indels
			0	Gaps
427	TTCTGTGTACTTGGCTGGCCCTCAACCGTCAAGGCTGCCACTGTGAGCTGCGCGCAGCC	486		
492	TTCTGTGTACTTGGCTGGCCCTCAACCGTCAAGGCTGCCACTGTGAGCTGCGCGCAGCC	433		
487	TGGCCCACTTCTGCACACAGCCTCCAGGGGCTGCTGTGGGACAGATTGCGGGCGTATGGCAG	546		
432	TGGCCCACTTCTGCACACAGCCTCCAGGGGCTGCTGTGGGACAGATTGCGGGCGTATGGCAG	373		
547	CTGTGGGCTACCCCACTGGCCCCAGCGGCTGTGGGACGTAAACCACTTGGACTTCCTGGCC	606		
372	CTGTGGGCTACCCCACTGGCCCCAGCGGCTGTGGGACGTAAACCACTTGGACTTCCTGGCC	313		
607	CTGCCACAGTGACTTCTCTCCAGAAAGATGAGAGCACTTGTGCTGTGAAGAGACTGCAGA	666		
312	CTGCCACAGTGACTTCTCTCCAGAAAGATGAGAGCACTTGTGCTGTGAAGAGACTGCAGA	253		
667	CTGTGGCTGTGGCGCTCTGGCCAAAGGACTTCAACCGGCTCAAGAAAGAGATGCAGCCTCCAG	726		
252	CTGTGGCTGTGGCGCTCTGGCCAAAGGACTTCAACCGGCTCAAGAAAGAGATGCAGCCTCCAG	193		
727	CAGCTGCAGTCAACCTGCACCTGGGGGGCTCATGGCTTTCGACTTTCGACTTCTCTCTT	786		
192	CAGCTGCAGTCAACCTGCACCTGGGGGGCTCATGGCTTTCGACTTTCGACTTCTCTCTT	133		
787	CGCTCCCTCC 795			
132	CGCTCCCTCC 124			

Query Match	33.8%	Score 269.4;	DB 10;	Length 283;
Best Local Similarity	99.3%	Pred. No. 1.2e-62;		
Matches 281; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1

```

RESULT 8
US-10-027-632-134702
Sequence 134702, Application US/10027652
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FaaiSeq for Windows Version 4.0

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SEQ ID NO 134702
LENGTH: 809
TYPE: DNA
ORGANISM: Human
US-10-027-632-134702

Query Match 22.1%; Score 175.8; DB 13; Length 809;
Best Local Similarity 86.9%; Pred. No. 1.7e-37;
Matches 192; Conservative 1; Mismatches 28; Indels 0; Gaps 0;

QY 66 CCGGCGCGGCGCCAGCCCGCCATGACCTCCGAGGAGGAGGAGCTCGGGGGAGTTA 125
DB 17 CCGGCGCGGCGCGCTATGCTTCTGTCATCTGCGCAGGGGAGCTCGGGGGAGTTA 76
QY 126 GCGTGCCTGTGACAGGCTGTGCTGAGCACTCCCTGACGATCCAGCTCTCAATGCACAGG 185
DB 77 GCGTGCCTGTGACAGGCTGTGCTGAGCACTCCCTGACGATCCAGCTCTCAATGCACAGG 136
QY 186 GACCCAGGCGCTGGCCCTTCATCCAGAAACCTATGACCTCACCGGCTACCTGAGAC 245
DB 137 GACCCAGGCGCTGGCCCTTCATCCAGAAACCTATGACCTCACCGGCTACCTGAGAC 196
QY 246 CACTCCGAGCTGGCTGGGAGCTTCTGACTGACTGGG 286
DB 197 CACTCCGAGCTGGCTGGGAGCTTCTGACTGACTGGG 237

RESULT 9
US-10-027-632-134702

Sequence 134702, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 134702
LENGTH: 809
TYPE: DNA
ORGANISM: Human
US-10-027-632-134702

Query Match 22.1%; Score 175.8; DB 14; Length 809;
Best Local Similarity 86.9%; Pred. No. 1.7e-37;
Matches 192; Conservative 1; Mismatches 28; Indels 0; Gaps 0;

QY 66 CCGGCGCGGCGCCAGCCCGCCATGACCTCCGAGGAGGAGGAGCTCGGGGGAGTTA 125
DB 17 CCGGCGCGGCGCGCTATGCTTCTGTCATCTGCGCAGGGGAGCTCGGGGGAGTTA 76
QY 126 GCGTGCCTGTGACAGGCTGTGCTGAGCACTCCCTGACGATCCAGCTCTCAATGCACAGG 185
DB 77 GCGTGCCTGTGACAGGCTGTGCTGAGCACTCCCTGACGATCCAGCTCTCAATGCACAGG 136
QY 186 GACCCAGGCGCTGGCCCTTCATCCAGAAACCTATGACCTCACCGGCTACCTGAGAC 245
DB 197 CACTCCGAGCTGGCTGGGAGCTTCTGACTGACTGGG 237

DB 137 GACCCAGGCGCGGCGCCCTTCATCCAGAAACCTATGACCTCACCGGCTACCTGAGAC 196
QY 246 CACTCCGAGCTGGCTGGGAGCTTCTGACTGACTGGG 286
DB 197 CACTCCGAGCTGGCTGGGAGCTTCTGACTGACTGGG 237

RESULT 10
US-10-212-793-7

Sequence 7, Application US/10212793
Publication No. US2003008795A1
GENERAL INFORMATION:
APPLICANT: Shi et al.
TITLE OF INVENTION: Cardiotrophin-like Cytokine
FILE REFERENCE: P385D1
CURRENT APPLICATION NUMBER: US/10/212,793
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 09/438,299
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/106,182
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: US 60/051,311
PRIOR FILING DATE: 1997-06-30
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 7

LENGTH: 396
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: Site
LOCATION: (199)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (293)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (306)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (360)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (371)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (377)
OTHER INFORMATION: n equals any nucleotide
FEATURE:
NAME/KEY: Site
LOCATION: (383)
OTHER INFORMATION: n equals any nucleotide
US-10-212-793-7

Query Match 10.1%; Score 80.2; DB 15; Length 396;
Best Local Similarity 96.5%; Pred. No. 7e-12;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 711 AAGATGACGCTTCCAGAGCTGACGCTGACCTGACCTGGGGGCTCAGGCTTCTGACTT 770
DB 4 AAGAGGAGGCTTCCAGAGCTGACGCTGACCTGACCTGGGGGCTCAGGCTTCTGACTT 63
QY 771 CTGACCTTCTCTCTGCTGCTCCCG 795
DB 64 CTGACCTTCTCTCTGCTGCTCCCG 88

RESULT 11
US-09-908-975-29446

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? Sequence 29446, Application US/09908975
? Publication No. US20030165843A1
? GENERAL INFORMATION:
? APPLICANT: SHOSHAN, Avi
? APPLICANT: WASSERMAN, Alon
? APPLICANT: MINTZ, Eli
? APPLICANT: MINTZ, Liat
? APPLICANT: FAIGLER, Shmchon
? TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICED
? TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
? FILE REFERENCE: 36688-0005
? CURRENT APPLICATION NUMBER: US/09/908,975
? CURRENT FILING DATE: 2001-07-20
? PRIOR APPLICATION NUMBER: US 60/287,724
? PRIOR FILING DATE: 2001-05-02
? PRIOR APPLICATION NUMBER: US 60/221,607
? PRIOR FILING DATE: 2000-07-28
? NUMBER OF SEQ ID NOS: 32337
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 29446
? LENGTH: 65
? TYPE: DNA
? ORGANISM: Mus musculus
? US-09-908-975-29446

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Query Match	7.4%	Score 58.6	DB 13	Length 65
Best Local Similarity	93.8%	Pred. No. 3.8e-06		
Matches	61	Conservative	0	Mismatches 4
				Indels 0
				Gaps 0

Oy 651 CTGAAGAGCTGCAGACTGGTGTGGCGCTGGCCAAAGACTTCAACCGGCTCAAGAG 710
 Db 1 CTGAAGAGCTGCAGACTGGCTATGGCGTTACGCAAGACTTCAACCGGCTTAAAG 60

Qy	711	AAGAT	715
Db	61	AAGAT	65

RESULT 12
US-10-102

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1 Sequence 266, Application No.10102806
2 Publication No. US20030054421A1
3
4 GENERAL INFORMATION:
5
6 APPLICANT: Rosen et al.
7 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
8 FILE REFERENCE: PA103P1C1
9 CURRENT APPLICATION NUMBER: US/10/102,806
10 CURRENT FILING DATE: 2002-03-22
11 PRIOR APPLICATION NUMBER: 09/925,298
12 PRIOR FILING DATE: 2001-09-10
13 PRIOR APPLICATION NUMBER: PCT/US00/05881
14 PRIOR FILING DATE: 2000-03-08
15 PRIOR APPLICATION NUMBER: 60/124,270
16 PRIOR FILING DATE: 1999-03-12
17 NUMBER OF SEQ ID NOS: 846
18 SOFTWARE: Patencin Ver. 2.0
19 SEQ ID NO 266
20 LENGTH: 2320
21
22 TYPE: DNA
23 ORGANISM: Homo sapiens
24 US-10-102-806-266

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Query Match	5.9%;	Score 46.8;	DB 15;	Length 2320;
Best Local Similarity	46.2%;	Pred. No. 0.0071;		
Matches 156;	Conservative	0;	Mismatches 182;	Indels 0;
				Gaps 0

Qy' 1 CGCGGAGACGGCGCTCGCCCTCCACTCGGCACTCCGGGAAAGAGCCCGACCCGG 70
Db 64 CGCAGAGTCTTGGGAGACCCGGGCGCGGACCCGAGACGGCGCGACCGCTCCGG 123
Qy 71 CGGGCCAGGCCCGCCAGCTGAGACTCCGAGCAGGGGACTTGTGGGGAGATTGAGCTG 130
Db 124 CTTGCGGCGCGGACCGGCGCATAGGGGGCCCCCGCGCGTCTCCGCGCATCTCGGTTTCGGTC 183

QY 131 CCTGAGCAGGAGTCTGGACACTCCCTGCAGATGCAGTCTCAATTCGACACAGGGAGCC 111
Db 184 TCGGCTCGGAGCTTTTACGCCCCCGAGAAAGATTCCGCGCTGTGTGTGCCCCAAGCCC 243
QY 191 AGGGCTGGCCCCCTTCATCCAGAAAACCTATAGACTCACCCGCTACCTTGGAGCACCAACT 250
Db 244 AAAGTAAATCCCTTTCGGCCCGGGGACAGCAGAGCTCCCCCGGACCCGGGGGCCAGCG 303
QY 251 CCGCAGCTTGGCTGGGACCTATCTGAACTAACCTGGGCCCCCTTTCACAGAGCCAGACTT 310
Db 304 GCACAGATGGGCCCGGATGGGCGAGATTCCCCCGCGCCCCCGAAGACTTTCCTCCGCT 363
QY 311 CAACCCCTCCCGCTGGGGGACAGACTCTGGCCAGGG 348
Db 364 CCACCTCCCTTGTCTGGGAGATGGCAGCAATTCAGAGGG 401

RESULT 13
US-10-014-717-1

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Sequence 1, Application US/10014717
Publication No. US2002019278A1
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30562A
CURRENT APPLICATION NUMBER: US/10/014,717
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US/09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-10-014-717-1

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Query Match	5.6%;	Score 44.8;	DB 14;	Length 68750;
Best Local Similarity	50.0%;	Pred. No. 0.031;		
Matches 112; Conservative	0;	Mismatches 112;	Indels 0;	Gaps 0

QY	456	CAGGCTGCCA	CTGTCTAGCTGCGCGCGGAC	CTGGCCATTTCTGCACGACCTTCCAGGGC	515
Db	57992	CAGGTACCGGTGGGAGCGCGGGGAA	CTCTCGCGCCCTTCCGATTCACGCCCGGGC	58051	
QY	516	CTGCTGGGACAGACTTTCGGGCGT	CATGAGAGCTCTGGGCTTACCCATGCGCCGAGCGCTG	575	
Db	58052	GTGTGTGGCGGATTCGGGCGCGT	CAGAGACCCCGGCGAGTCCGACCTCGCCCGCCCTGGCC	58111	
QY	576	CTTGGAGCTGACCCCATTTGAACT	CTCTGCGCCCTGCCACAGTGA	CTTCTCCAGAAATG	635
Db	58112	GCCCGGCTTCATCCGCCCGCGCGCT	CGGCTATCTATGTGCGCTCGCGCAGATGGGG	58171	
QY	636	GAGACATTTCTGTGCTGTGAAGA	GCTGCAGACCTGTGCTGTGGCG	679	
Db	58172	CTTCCAAATACGGCCCGCGTTCGGGGGG	CTCGCGCACTGTGGCG	58215	

RESULT 14

Sequence 1127, Application US/10295027
Publication No. US2003023350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Atiz, Nacasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.


```
APPLICANT: Glyme, Richard
APPLICANT: Hevizi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT FILING DATE: 2002-11-13
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 3195
TYPE: DNA
ORGANISM: Homo sapiens
US-10-295-027-1127

Query Match      5.5%; Score 43.6; DB 12; Length 3195;
Best Local Similarity 44.3%; Pred. No. 0.053;
Matches 178; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 320 CCGCTGGGGGCAAGACTGCTGCCAGGCGCACTGTTGACTTGGAGGTGGCGAAGCT 379
DB 1328 CCACCTGGCCGGGTGGCTTGTGCGCAGGTCAAGTCATCGCGGTGCTGGCGCTCAGCTC 1387
QY 380 CAATGACAACACTGGCGCTGACCCAGAACTACGAGGCTACAGCCACTTGTGTACTT 439
DB 1388 GGTGACCGCGACCCGGGTGGCGGAGCATCTGTACTGTGGCAACGAGCCTGGAACAACCT 1447
QY 440 GCGTGGCTCAACCGTCAAGGCTGCGACTGTGAGTGGCGCGGCGGCGCCCACTTCTG 499
DB 1448 GCGCGGCTTCTGTCTGGGCGCGCTGTATCTACTCTTTCATGCGACCAATGTTCTCT 1507
QY 500 CACCACTTCAGAGGCTGCTGGGCGAGCATGCGGGCTCATGAGGCTGAGGCTACCC 559
DB 1508 GCGCGGCTTCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1567
QY 560 ACTGCGCCAGCGCGCTGCTGGAGCTGAACCACTTGAAGTCTGCGGCTGCGCCACAGTGA 619
DB 1568 CAAGACGCAAGAGCTGAGAAAGTATGATCGGCTGAGGCTGTTCACTGCTCTACAC 1627
QY 620 TTCTCTCAGAAGATGAGCACTTGTGCTGTGAAGAGCTGAGAGCTGCTGTGCG 679
DB 1628 GGTGCGCGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1687
QY 680 CTCGGCCAAAGACTTCAACCGGCTCAAGAAAGATGCGAGCC 721
DB 1688 GAGGCGCAAGCAACTGCGCGTGTGCTGCGGAGCTGCAAGCC 1729
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RESULT 15
US-10-285-976-54
Sequence 54, Application US/10285976
Publication No. US20030165500A1
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leoni, Lorenzo M.
APPLICANT: Corr, Maripat
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: In Head and Neck Squamous Cell Carcinomas
CURRENT FILING DATE: 2002-11-01
PRIOR FILING DATE: 2001-05-01
PRIOR FILING DATE: 2001-05-01
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 3195
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human frizzled8 (Fzd8)
US-10-285-976-54

Query Match      5.5%; Score 43.6; DB 13; Length 3195;
Best Local Similarity 44.3%; Pred. No. 0.053;
Matches 178; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 320 CCGCTGGGGGCAAGACTGCTGCCAGGCGCACTGTTGACTTGGAGGTGGCGAAGCT 379
DB 1328 CCACCTGGCCGGGTGGCTTGTGCGCAGGTCAAGTCATCGCGGTGCTGGCGCTCAGCTC 1387
QY 380 CAATGACAACACTGGCGCTGACCCAGAACTACGAGGCTACAGCCACTTGTGTACTT 439
DB 1388 GGTGACCGCGACCCGGGTGGCGGAGCATCTGTACTGTGGCAACGAGCCTGGAACAACCT 1447
QY 440 GCGTGGCTCAACCGTCAAGGCTGCGACTGTGAGTGGCGCGGCGGCGCCCACTTCTG 499
DB 1448 GCGCGGCTTCTGTCTGGGCGCGCTGTATCTACTCTTTCATGCGACCAATGTTCTCT 1507
QY 500 CACCACTTCAGAGGCTGCTGGGCGAGCATGCGGGCTCATGAGGCTGAGGCTACCC 559
DB 1508 GCGCGGCTTCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1567
QY 560 ACTGCGCCAGCGCGCTGCTGGAGCTGAACCACTTGAAGTCTGCGGCTGCGCCACAGTGA 619
DB 1568 CAAGACGCAAGAGCTGAGAAAGTATGATCGGCTGAGGCTGTTCACTGCTCTACAC 1627
QY 620 TTCTCTCAGAAGATGAGCACTTGTGCTGTGAAGAGCTGAGAGCTGCTGTGCG 679
DB 1628 GGTGCGCGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1687
QY 680 CTCGGCCAAAGACTTCAACCGGCTCAAGAAAGATGCGAGCC 721
DB 1688 GAGGCGCAAGCAACTGCGCGTGTGCTGCGGAGCTGCAAGCC 1729
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Search completed: February 9, 2004, 09:36:12
Job time : 369.674 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 06:10:20 / Search time 65.1015 Seconds
(without alignments)
5403.600 Million cell updates/sec

Title: US-09-931-704-1

Perfect score: 797

Sequence: 1 attaaagctcgcgcgagcc.....ctcctcttcgctccccc 797

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued Patents NA:
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2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	1	US-08-792-019B-1
2	797	100.0	797	3	US-08-988-819-1
3	797	100.0	797	3	US-09-016-534-1
4	749.4	94.0	1710	3	US-09-106-182-1
5	669.4	84.0	819	1	US-08-792-019B-4
6	669.4	84.0	819	3	US-08-988-819-4
7	669.4	84.0	819	3	US-09-016-534-4
8	523.4	65.7	5087	1	US-08-792-019B-3
9	523.4	65.7	5087	3	US-08-988-819-3
10	523.4	65.7	5087	3	US-09-016-534-3
11	80.2	10.1	396	3	US-09-106-182-7
12	44.8	5.6	68750	3	US-09-335-409-1
13	44.8	5.6	68750	4	US-09-568-102-1
14	44.8	5.6	68750	4	US-09-567-969-1
15	44.8	5.6	68750	4	US-09-568-480-1
16	44.8	5.6	68750	4	US-09-568-486-1
17	44.8	5.6	68750	4	US-09-568-472-1
18	44.8	5.6	68750	4	US-09-567-899-1
19	42.2	5.3	1590	4	US-09-252-991A-10070
20	42.2	5.3	1878	4	US-09-252-991A-9765
21	38.6	4.8	6858	4	US-09-252-991A-1219
22	38.4	4.8	71989	4	US-09-443-501A-2
23	38	4.8	223	1	US-08-383-761-1
24	38	4.8	223	1	US-08-824-277-1
25	37.8	4.7	3129	3	US-09-387-695-1
26	37.8	4.7	49272	1	US-08-614-770A-1
27	37.6	4.7	1071	4	US-09-252-991A-14206

C	28	37.6	4.7	2388	4	US-09-252-991A-14064	Sequence 14064, A
	29	37.4	4.7	900	4	US-09-252-991A-9282	Sequence 9282, Ap
	30	37.4	4.7	3729	4	US-09-252-991A-9272	Sequence 9272, Ap
C	31	37.2	4.7	1242	4	US-09-252-991A-9668	Sequence 9668, Ap
	32	37.2	4.7	1521	4	US-09-252-991A-9746	Sequence 9746, Ap
	33	37.2	4.7	2511	4	US-09-252-991A-9494	Sequence 9494, Ap
	34	37.2	4.7	3583	4	US-09-252-991A-9541	Sequence 9541, Ap
C	35	37.2	4.7	3984	4	US-09-016-434-1199	Sequence 1199, Ap
	36	37.2	4.6	468	4	US-09-252-991A-3528	Sequence 3528, Ap
	37	37	4.6	1449	4	US-09-252-991A-3558	Sequence 3558, Ap
	38	37	4.6	1698	4	US-09-252-991A-3551	Sequence 3551, Ap
C	39	37	4.6	2196	4	US-09-252-991A-3536	Sequence 3536, Ap
	40	36.8	4.6	336	4	US-09-252-991A-12979	Sequence 12979, A
	41	36.8	4.6	1059	4	US-09-252-991A-12662	Sequence 12662, A
	42	36.8	4.6	1308	4	US-08-937-067-18	Sequence 18, Appl
	43	36.8	4.6	2075	4	US-09-087-031E-2	Sequence 2, Appl
	44	36.8	4.6	2078	4	US-09-087-031E-1	Sequence 1, Appl
	45	36.8	4.6	2124	4	US-09-087-031E-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-792-019B-1
Sequence 1, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUTROPHILIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: AMGEN INC.
STREET: 1640 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE FOR SEQ ID NO: 1:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
NAME/KEY: CDS
LOCATION: 90..764
FEATURE: mat_peptide
NAME/KEY: 171..764
LOCATION: 171..764
FEATURE: sig_peptide
NAME/KEY: sig_peptide
LOCATION: 90..170
US-08-792-019B-1
Query Match 100.0%; Score 797; DB 1; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.7e-181;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTAAGCTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 60
DB 1 ATTAAGCTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 60
QY 61 CCGGACCCGCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 120
DB 61 CCGGACCCGCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 120
QY 121 TGTAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTG 180
DB 121 TGTAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTG 180
QY 181 CAGGGGAGCCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 240
DB 181 CAGGGGAGCCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 240
QY 241 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 300
DB 241 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 300
QY 301 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 360
DB 301 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 360
QY 361 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 420
DB 361 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 420
QY 421 GGCACCTTGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTG 480
DB 421 GGCACCTTGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTG 480
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DB 541 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 600
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DB 601 CTGGGCTTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAG 660
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DB 661 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 720
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QY 781 CCTTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAG 797
DB 781 CCTTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAG 797

RESULT 2

US-08-988-819-1
; Sequence 1 Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:

QY 1 ATTAAGCTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 60
DB 1 ATTAAGCTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 60
QY 61 CCGGACCCGCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 120
DB 61 CCGGACCCGCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 120
QY 121 TGTAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAG 180
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QY 181 CAGGGGAGCCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 240
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DB 241 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 300
QY 301 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 360
DB 301 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 360
QY 361 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 420
DB 361 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCACTCCGCCAGCCTCCGGAGAGAG 420
QY 421 GGCACCTTGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAG 480
DB 421 GGCACCTTGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAG 480
QY 481 GGAGCTTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTG 540
DB 481 GGAGCTTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTGCTGAGCGTGTG 540

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988, 819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..764
FEATURE:
NAME/KEY: mat peptide
LOCATION: 171..764
NAME/KEY: sig peptide
LOCATION: 90..170
US-08-988-819-1

Query Match 100.0%; Score 797; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 4,7e-181;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 541 TGGCAGCTCTGGGCTACCACTGCGCCGACGCGCTGCTGGGACTGAGACCACTTGGAGCTC 600
DB 541 TGGCAGCTCTGGGCTACCACTGCGCCGACGCGCTGCTGGGACTGAGACCACTTGGAGCTC 600
QY 601 CTGGCCCTGCGCCAGAGTGAATCTTCTCTCAGAGATGAGAGCACTTCTGGCTGCTGAAGAGC 660
DB 601 CTGGCCCTGCGCCAGAGTGAATCTTCTCTCAGAGATGAGAGCACTTCTGGCTGCTGAAGAGC 660
QY 661 TGCAGACCTGGGCTGCGGCTGCGGCGCAAGAGACTTCAACCGGCTCAAGAGAGATGAGAGC 720
DB 661 TGCAGACCTGGGCTGCGGCTGCGGCGCAAGAGACTTCAACCGGCTCAAGAGAGATGAGAGC 720
QY 721 CTCGACGAGCTGACGACCTGCACTGCGGCGCTGATGAGCTTCTGACTTCTGACCTTCT 780
DB 721 CTCGACGAGCTGACGACCTGCACTGCGGCGCTGATGAGCTTCTGACTTCTGACCTTCT 780
QY 781 CCTCTTGGCTCCCCC 797
DB 781 CCTCTTGGCTCCCCC 797

RESULT 3

US-09-016-534-1
Sequence 1, Application us/09016534
Patent No. 6143874

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI
APPLICANT: ELIOTT, GARY S.
APPLICANT: SARMENTO, ULIA
APPLICANT: SERALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS
LOCATION: 90..764

NAME/KEY: mat_peptide
LOCATION: 171..764

NAME/KEY: sig_peptide
LOCATION: 90..170

US-09-016-534-1

Query Match 100.0%; Score 797; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 4,7e-181;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTAAGCTTGGCGGAGCCGCGCTGCGCTCCCACTCCGCGAGAGAGAG 60
DB 1 ATTAAGCTTGGCGGAGCCGCGCTGCGCTCCCACTCCGCGAGAGAGAG 60
QY 61 CCGACCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 61 CCGACCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 TGTAGCGTGTGCTGAGCGGTGCTGAGCGAGCTTCCCTGAGTGCAGCTCAATCCGA 180
DB 121 TGTAGCGTGTGCTGAGCGGTGCTGAGCGAGCTTCCCTGAGTGCAGCTCAATCCGA 180
QY 181 CAGGGGACCCAGGGGCTGGGCGCTTCATCAGAAAACCTATGACTCCGCGTACCTGG 240
DB 181 CAGGGGACCCAGGGGCTGGGCGCTTCATCAGAAAACCTATGACTCCGCGTACCTGG 240
QY 241 AGCACCACTCCGAGCTTGGCTGGAGCTATCTGAATACCTGAGCCCTTTCAACG 300
DB 241 AGCACCACTCCGAGCTTGGCTGGAGCTATCTGAATACCTGAGCCCTTTCAACG 300
QY 301 AGCCAGACTTCAACCTCCCGCGCTGGGGGAGAGACTCTGCCAGGGGCACTGTTGACT 360
DB 301 AGCCAGACTTCAACCTCCCGCGCTGGGGGAGAGACTCTGCCAGGGGCACTGTTGACT 360
QY 361 TGGAGGTGCGGAGAGCTCAATGACAACTGCGGCTGAGCCAGAACTACGAGGCTTCA 420
DB 361 TGGAGGTGCGGAGAGCTCAATGACAACTGCGGCTGAGCCAGAACTACGAGGCTTCA 420
QY 421 GCCACTTCTGTGTACTTGTGCTGCTGAGCTTCAACCGTCAAGGCTGCTGAGTGGCGC 480
DB 421 GCCACTTCTGTGTACTTGTGCTGCTGAGCTTCAACCGTCAAGGCTGCTGAGTGGCGC 480
QY 481 GAGGCTGCGGCACTTCTGAGCAGGCTCAGGGGCTGCTGGGAGCATGCGGGGCTCA 540
DB 481 GAGGCTGCGGCACTTCTGAGCAGGCTCAGGGGCTGCTGGGAGCATGCGGGGCTCA 540
QY 541 TGGCAGCTCTGGGCTACCACTGCGCCGACGCGCTGCTGGGACTGAGACCACTTGGAGCTC 600
DB 541 TGGCAGCTCTGGGCTACCACTGCGCCGACGCGCTGCTGGGACTGAGACCACTTGGAGCTC 600
QY 601 CTGGCCCTGCGCCAGAGTGAATCTTCTCTCAGAGATGAGAGCACTTCTGGCTGCTGAAGAGC 660
DB 601 CTGGCCCTGCGCCAGAGTGAATCTTCTCTCAGAGATGAGAGCACTTCTGGCTGCTGAAGAGC 660
QY 661 TGCAGACCTGGGCTGCGGCTGCGGCGCAAGAGACTTCAACCGGCTCAAGAGAGATGAGAGC 720
DB 661 TGCAGACCTGGGCTGCGGCTGCGGCGCAAGAGACTTCAACCGGCTCAAGAGAGATGAGAGC 720
QY 721 CTCGACGAGCTGACGACCTGCACTGCGGCGCTGATGAGCTTCTGACTTCTGACCTTCT 780
DB 721 CTCGACGAGCTGACGACCTGCACTGCGGCGCTGATGAGCTTCTGACTTCTGACCTTCT 780
QY 781 CCTCTTGGCTCCCCC 797
DB 781 CCTCTTGGCTCCCCC 797

RESULT 4

US-09-106-182-1
Sequence 1, Application us/09106182
Patent No. 6046035

GENERAL INFORMATION:

APPLICANT: Shi, Yangu
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Cardiotrophin-Like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave

CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF385
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1710 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 46..720
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 46..126
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 127..720
US-09-106-182-1

Query Match 94.0%; Score 749.4; DB 3; Length 1710;
Best Local Similarity 99.9%; Pred. No. 1.2e-169;
Matches 750; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

45 GGCCTCCGGAGAGAGCCGACCCGCGCCGAGCCGACCCGACCTGAGCACTCCGAGCA 104
1 GGCCTCCGGAGAGAGCCGACCCGCGCCGAGCCGACCCGACCTGAGCACTCCGAGCA 60
105 GGGAGACTCGTGGGGGATGTTAGCGTGCCTGTGCAAGGCTCTGAGCACTCCGAGCA 164
61 GGGAGACTCGTGGGGGATGTTAGCGTGCCTGTGCAAGGCTCTGAGCACTCCGAGCA 120
165 CCAAGCTCTCAATGCAAGAGGAGCCGAGGAGGCTGAGGCTCTCAATGCAAGGAGG 224
121 CCAAGCTCTCAATGCAAGAGGAGCCGAGGAGGCTGAGGCTCTCAATGCAAGGAGG 180
225 CTCACCCGCTACCTGAGAGCACTCCGAGGCTGAGGAGGCTCTCAATGCAAGGAGG 284
181 CTCACCCGCTACCTGAGAGCACTCCGAGGCTGAGGAGGCTCTCAATGCAAGGAGG 240
285 GAGCCGCTCTTCAACAGAGCAGACTTCAACCTCCGCGCTGAGGAGCAGAGACTGAGCC 344
241 GAGCCGCTCTTCAACAGAGCAGACTTCAACCTCCGCGCTGAGGAGCAGAGACTGAGCC 300
345 AGGGCCACTGTGACTTGGAGGTGTGGCGAAGCTTCAATGAGAACTGCGGCTGAGCCAG 404
301 AGGGCCACTGTGACTTGGAGGTGTGGCGAAGCTTCAATGAGAACTGCGGCTGAGCCAG 360
405 AACTAGAGAGGCTTCAAGCACTTCTGTGTACTTGTGCGTGAACCTGAGGCTGCC 464
361 AACTAGAGAGGCTTCAAGCACTTCTGTGTACTTGTGCGTGAACCTGAGGCTGCC 420

465 ACTGCTGAGCTGCGCCGAGCCTGAGCCTTCTGACACAGGCTTCAAGGAGGCTGAGGC 524
421 ACTGCTGAGCTGCGCCGAGCCTGAGCCTTCTGACACAGGCTTCAAGGAGGCTGAGGC 480
525 AGCATTTGGGGGCTGATGAGCTGAGGCTTGAAGCCACTGAGCCGAGGCTGAGGACT 584
481 AGCATTTGGGGGCTGATGAGCTGAGGCTTGAAGCCACTGAGCCGAGGCTGAGGACT 540
595 GAACCCACTTGGAGCTTCCGCGCCGAGCAGTGAAGCTTCTGAGAGAGTGAAGAGACTTC 644
541 GAACCCACTTGGAGCTTCCGCGCCGAGCAGTGAAGCTTCTGAGAGAGTGAAGAGACTTC 600
645 TGGCTGTGAAGAGAGCTGAGCAGCTGAGTGTGGCGCTGAGGCAAGAGCTTGAACCGGCTC 704
601 TGGCTGTGAAGAGAGCTGAGCAGCTGAGTGTGGCGCTGAGGCAAGAGCTTGAACCGGCTC 660
705 AAGAGAAAGTGAAGAGCTTCAAGAGCTGAGTGAAGTGAAGCTTGAAGCTGAGGAGCTTTC 764
661 AAGAGAAAGTGAAGAGCTTCAAGAGCTGAGTGAAGTGAAGCTTGAAGCTGAGGAGCTTTC 720
765 TGACTTGAAGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
721 TGACTTGAAGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751

RESULT 5
US-08-792-0198-4
Sequence 4, Application US/087920198
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,0198
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 95..769
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 176..769
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 95..175
US-08-792-0198-4

Query Match 84.0%; Score 669.4; DB 1; Length 819;
Best Local Similarity 92.0%; Pred. No. 1.1e-150;

Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCGCGAGCTCGGGAGAGAG 60
Db 5 ATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCGCGAGCTCGGGAGAGAG 64

QY 61 CCGCAGCCGCGCGCGAG-CGCCAGGCCCATGAGACTCCGAGCAGGGGAGCTGCGGG 119
Db 65 CCGGCGCCG 124

QY 120 ATGTAGCGTCTGTGCAAGGTCTGTGCAAGCTCTCTGCAAGTGGCACTTCAATCC 179
Db 125 ATGTAGCTTGTCTGTGCAAGGTCTGTGCAAGCTCTCTGCAAGTGGCACTTCAATCC 184

QY 180 ACAGGGAGCCGAGGCGCTGCGCTCCATCGAGAACTATGACCTACCGGCTACCTG 239
Db 185 ACAGGAGATCGAGGCGCTGCGCTCCATCGAGAACTATGACCTACCGGCTACCTG 244

QY 240 GAGCAGCACTCGCGAGCTTGGCTGGAGCTATCTGAATACCTGGGCGCGCTTCAAC 239
Db 245 GAGCATCACTCGCGAGCTTAGCTGGGAGCTTACCTGAATACCTGGGCGCGCTTCAAC 304

QY 300 GAGCAGCACTTCAACCTCCCGCGCTGGGGGAGAGACTCTGCCAGGGCGCTATTGAC 359
Db 305 GAGCCTGACTTCAATCTCTCGACTGGGGGAGAACTCTGCCAGGGCGCGCTCAAC 364

QY 360 TTGGAGGTGGGAGAGCTCAATGAACTGCGGTGACCGAGAACTAGCGAGGCTAC 419
Db 365 TTGGAGGTGGGAGAGCTCAATGAACTGCGGTGACCGAGAACTAGCGAGGCTAC 424

QY 420 AGCCAGCTTGTGTACTGTGCGCTGAGCTCAACCGTCAAGCTGCGCACTGCTGAGCTGCG 479
Db 425 AGTCACTCTGTGTACTGTGCGCTGAGCTCAACCGTCAAGCTGCGCACTGCTGAGCTGCG 484

QY 480 CGAGAGCTTGGCCCACTTCTGCAAGCTTCAAGGCTCTGCTGGGAGAGATTTGGGGGCTG 539
Db 485 CGTAGCTTGGCCCACTTCTGCAAGCTTCAAGGCTCTGCTGGGAGAGATTTGGGGGCTG 544

QY 540 ATGGAGCTTGGGCTTACCACTGCGCGCGCGCGCGCTGCTGGGAGAGATTTGGGGGCTG 599
Db 545 ATGGAGCTTGGGCTTACCACTGCGCGCGCGCGCGCTGCTGGGAGAGATTTGGGGGCTG 604

QY 600 CTTGCGCTGCGCGAGCTTCTCTCAGAGAGTGAAGCACTTCTGCTGCTGAGAGAG 659
Db 605 CTTGCGCTGCGCGAGCTTCTCTCAGAGAGTGAAGCACTTCTGCTGCTGAGAGAG 664

QY 660 CTGCAAGCTTGGCTGTGGCGCTCGCGAGAGACTTCAACCGGCTCAAGAGAGATGACAG 719
Db 665 CTGCAAGCTTGGCTGTGGCGCTCGCGAGAGACTTCAACCGGCTCAAGAGAGATGACAG 724

QY 720 CTTCCAGAGCTGAGTCAAGCTTCTGCAAGCTTGGGGGCTATGAGCTTCTGAGCTT 778
Db 725 CTTCCAGAGCTTCAAGTCAAGCTTCTGCAAGCTTGGGGGCTATGAGCTTCTGAGCTT 783

RESULT 6
US-08-988-819-4
Sequence 4, Application US/0898819
Patent No. 6054294

GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 95..769
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 176..769
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 95..175
US-08-988-819-4

Query Match 84.0%; Score 669.4; DB 3; Length 819;
Best Local Similarity 92.0%; Pred. No. 1.1e-150;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCGCGAGCTCGGGAGAGAG 60
Db 5 ATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCGCGAGCTCGGGAGAGAG 64

QY 61 CCGCAGCCGCGCGCGAG-CGCCAGGCCCATGAGACTCCGAGCAGGGGAGCTGCGGG 119
Db 65 CCGGCGCCG 124

QY 120 ATGTAGCGTCTGTGCAAGGTCTGTGCAAGCTCTCTGCAAGTGGCACTTCAATCC 179
Db 125 ATGTAGCTTGTCTGTGCAAGGTCTGTGCAAGCTCTCTGCAAGTGGCACTTCAATCC 184

QY 180 ACAGGGAGCCGAGGCGCTGCGCTCCATCGAGAACTATGACCTACCGGCTACCTG 239
Db 185 ACAGGAGATCGAGGCGCTGCGCTCCATCGAGAACTATGACCTACCGGCTACCTG 244

QY 240 GAGCAGCACTCGCGAGCTTGGCTGGAGCTATCTGAATACCTGGGCGCGCTTCAAC 239
Db 245 GAGCATCACTCGCGAGCTTAGCTGGGAGCTTACCTGAATACCTGGGCGCGCTTCAAC 304

QY 300 GAGCAGCACTTCAACCTCCCGCGCTGGGGGAGAGACTCTGCCAGGGCGCTATTGAC 359
Db 305 GAGCCTGACTTCAATCTCTCGACTGGGGGAGAACTCTGCCAGGGCGCGCTCAAC 364

QY 360 TTGGAGGTGGGAGAGCTCAATGAACTGCGGTGACCGAGAACTAGCGAGGCTAC 419
Db 365 TTGGAGGTGGGAGAGCTCAATGAACTGCGGTGACCGAGAACTAGCGAGGCTAC 424

QY 420 AGCCAGCTTGTGTACTGTGCGCTGAGCTCAACCGTCAAGCTGCGCACTGCTGAGCTGCG 479
Db 425 AGTCACTCTGTGTACTGTGCGCTGAGCTCAACCGTCAAGCTGCGCACTGCTGAGCTGCG 484

QY 480 CGAGAGCTTGGCCCACTTCTGCAAGCTTCAAGGCTCTGCTGGGAGAGATTTGGGGGCTG 539
Db 485 CGTAGCTTGGCCCACTTCTGCAAGCTTCAAGGCTCTGCTGGGAGAGATTTGGGGGCTG 544

QY 540 ATGGAGCTTGGGCTTACCACTGCGCGCGCGCGCGCTGCTGGGAGAGATTTGGGGGCTG 599

Db 545 ATGGCGACGCTTGGCTAACCCTGCCCCGACCTCTGCGAGGGACTGAGCCAGGCTGGGCC 604
Qy 600 CTGGGCGCTGCCACAGTACTTCTCCAGAAAGATGAGCACTTGGGCTGTAAGGAG 659
Db 605 CTGGGCGCTGCCACAGTACTTCTCCAGAAAGATGAGCACTTGGGCTGTAAGGAG 664
Qy 660 CTGGGCGCTGCCACAGTACTTCTCCAGAAAGATGAGCACTTGGGCTGTAAGGAG 719
Db 665 CTGGGCGCTGCCACAGTACTTCTCCAGAAAGATGAGCACTTGGGCTGTAAGGAG 724
Qy 720 CTGGGCGCTGCCACAGTACTTCTCCAGAAAGATGAGCACTTGGGCTGTAAGGAG 778
Db 725 CTGGGCGCTGCCACAGTACTTCTCCAGAAAGATGAGCACTTGGGCTGTAAGGAG 783

RESULT 7
US-09-016-534-4
Sequence 4, Application US/09016534
Patent No. 613874
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: ELLIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 95..769
NAME/KEY: mat_peptide
LOCATION: 176..769
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 95..175
US-09-016-534-4

Query Match 84.0%; Score 669.4; DB 3; Length 819;
Best Local Similarity 92.0%; Pred. No. 1.1e-150;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
1 ATTAAAGCTTCGCGAGGCGGCGCTGCGCTCCCACTCCGCGAGGCTTCGCGAGGAG 60
|||||

Db 5 ATTAAAGCTTCGCGAGGCGGCGCTGCGCTCCCACTCCGCGAGGCTTCGCGAGGAG 64
Qy 61 CGGACCGGCGCGGCGCGAG-CCCGAGCCCAATGACCTCCGAGGAGGAGGACTGCGGAGG 119
Db 65 CGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGG 124
Qy 120 ATGTTAGCTGCTGACGAGGCTGCTGAGCACTTCCCTGAGTGCAGCTTCAATGCG 179
Db 125 ATGTTAGCTGCTGACGAGGCTGCTGAGCACTTCCCTGAGTGCAGCTTCAATGCG 184
Qy 180 ACAGGAGACCCAGGCGCTGCGGCTGCTGATCCAGAAACCTTATGACTTACCTGACTG 239
Db 185 ACAGGAGATCCAGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 244
Qy 240 GAGCACAATCCGAGCTGGCTGGGAGCTATGAACTTCCCTGAGGCGGCGGCGGCGG 299
Db 245 GAGCACAATCCGAGCTGGCTGGGAGCTATGAACTTCCCTGAGGCGGCGGCGGCGG 304
Qy 300 GAGCACAATCCGAGCTGGCTGGGAGCTATGAACTTCCCTGAGGCGGCGGCGGCGG 359
Db 305 GAGCACAATCCGAGCTGGCTGGGAGCTATGAACTTCCCTGAGGCGGCGGCGGCGG 364
Qy 360 TTGAGGCTGGGCGGAGCTTCAATGACAACTGCGGCTGAGCCAGAACTTACGAGGCTTAC 419
Db 365 TTGAGGCTGGGCGGAGCTTCAATGACAACTGCGGCTGAGCCAGAACTTACGAGGCTTAC 424
Qy 420 AGGCACTTGTGTGTTACTTGGGAGCTTCAACGCTGAGGCGGCGGCGGCGGCGG 479
Db 425 AGTCACTTGTGTGTTACTTGGGAGCTTCAACGCTGAGGCGGCGGCGGCGGCGG 484
Qy 480 CGGACCTGGGCGGAGCTTGGAGCAAGGCTTCCAGGAGGCTGCTGGGAGGAGTGGGCGG 539
Db 485 CGTACCTGGGCGGAGCTTGGAGCAAGGCTTCCAGGAGGCTGCTGGGAGGAGTGGGCGG 544
Qy 540 ATGCACTTGGGCTTGGAGCAAGGCTTCCAGGAGGCTGCTGGGAGGAGTGGGCGG 599
Db 545 ATGCACTTGGGCTTGGAGCAAGGCTTCCAGGAGGCTGCTGGGAGGAGTGGGCGG 604
Qy 600 CTGGGCGGCGGCGGAGGAGCTTCCAGGAGGAGTGGAGTGGCTGCTGTAAGGAG 659
Db 605 CTGGGCGGCGGCGGAGGAGCTTCCAGGAGGAGTGGAGTGGCTGCTGTAAGGAG 664
Qy 660 CTGGGCGGCGGCGGAGGAGCTTCCAGGAGGAGTGGAGTGGCTGCTGTAAGGAG 719
Db 665 CTGGGCGGCGGCGGAGGAGCTTCCAGGAGGAGTGGAGTGGCTGCTGTAAGGAG 724
Qy 720 CTGGGCGGCGGCGGAGGAGCTTCCAGGAGGAGTGGAGTGGCTGCTGTAAGGAG 778
Db 725 CTGGGCGGCGGCGGAGGAGCTTCCAGGAGGAGTGGAGTGGCTGCTGTAAGGAG 783

RESULT 8
US-08-792-019B-3
Sequence 3, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B

FILING DATE: 03-FEB-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: COOK, ROBERT R.
 REGISTRATION NUMBER: 31,602
 REFERENCE/DOCKET NUMBER: A-442
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5087 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: 137..138
 OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED
 OTHER INFORMATION: REGION OF >1KB"
 US-08-792-019B-3

Query Match 65.7%; Score 523.4; DB 1; Length 5087;
 Best Local Similarity 99.8%; Pred. No. 1e-115; Indels 0; Gaps 0;
 Matches 524; Conservative 0; Mismatches 1;

271 ATCTGAATCACTGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGGCTGGGG 330
 3363 AGCTGAATCACTGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGGCTGGGG 3422
 331 CAGAGACTCTGCGCCAGGCGCACTGTGACTTGGAGGTGTGGCGAACCTTCATGACAAAC 390
 3423 CAGAGACTCTGCGCCAGGCGCACTGTGACTTGGAGGTGTGGCGAACCTTCATGACAAAC 3482
 391 TGGGCTGACCCAGAACTACGAGGCTTACAGCCACTTCTGTGTTACTTGGCGGCTCA 450
 3483 TGGGCTGACCCAGAACTACGAGGCTTACAGCCACTTCTGTGTTACTTGGCGGCTCA 3542
 451 ACCGTGAGCTGCGCACTGTGAGCTGCGCGAGCTTGGCGCACTTCTGCAACGAGCTCC 510
 3543 ACCGTGAGCTGCGCACTGTGAGCTGCGCGAGCTTGGCGCACTTCTGCAACGAGCTCC 3602
 511 AGGCGCTGCTGGGACAGCTTGGGCGGTCAATGGACCTTGGGCTAACCACTGCCCCAGC 570
 3603 AGGCGCTGCTGGGACAGCTTGGGCGGTCAATGGACCTTGGGCTAACCACTGCCCCAGC 3662
 571 CGCTGCTGGGAGTGAACCACTTGAATCTCTGCGCCCTGCGCCAGATGACTTCTCCAGA 630
 3663 CGCTGCTGGGAGTGAACCACTTGAATCTCTGCGCCCTGCGCCAGATGACTTCTCCAGA 3722
 631 AGATGACGACTTCTGAGCTGCTGAAGAGCTGACAGCTGAGCTGTGGCGCTGGCCAGG 690
 3723 AGATGACGACTTCTGAGCTGCTGAAGAGCTGACAGCTGAGCTGTGGCGCTGGCCAGG 3782
 691 ACTTCAACCGGCTCAAGAGAGATGACAGCTTCAAGAGCTGACAGCTTCAAGAGCTGAG 750
 3783 ACTTCAACCGGCTCAAGAGAGATGACAGCTTCAAGAGCTGACAGCTTCAAGAGCTGAG 3842
 751 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTTCTGCTCCCTCC 795
 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTTCTGCTCCCTCC 3887

RESULT 9
 US-08-988-819-3
 Sequence 3, Application US/08988819
 Patent No. 6054294
 GENERAL INFORMATION:
 APPLICANT: CHANG, MING-SHI
 TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AMGEN INC.
 STREET: ONE AMGEN CENTER DRIVE
 CITY: THOUSAND OAKS

STATE: CA
 COUNTRY: USA
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,819
 FILING DATE: 12-DEC-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/792,019
 FILING DATE: 03-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: COOK, ROBERT R.
 REGISTRATION NUMBER: 31,602
 REFERENCE/DOCKET NUMBER: A-442A
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5087 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: 137..138
 OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED
 OTHER INFORMATION: REGION OF >1KB"
 US-08-988-819-3

Query Match 65.7%; Score 523.4; DB 3; Length 5087;
 Best Local Similarity 99.8%; Pred. No. 1e-115; Indels 0; Gaps 0;
 Matches 524; Conservative 0; Mismatches 1;

271 ATCTGAATCACTGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGGCTGGGG 330
 3363 AGCTGAATCACTGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGGCTGGGG 3422
 331 CAGAGACTCTGCGCCAGGCGCACTGTGACTTGGAGGTGTGGCGAACCTTCATGACAAAC 390
 3423 CAGAGACTCTGCGCCAGGCGCACTGTGACTTGGAGGTGTGGCGAACCTTCATGACAAAC 3482
 391 TGGGCTGACCCAGAACTACGAGGCTTACAGCCACTTCTGTGTTACTTGGCGGCTCA 450
 3483 TGGGCTGACCCAGAACTACGAGGCTTACAGCCACTTCTGTGTTACTTGGCGGCTCA 3542
 451 ACCGTGAGCTGCGCACTGTGAGCTGCGCGAGCTTGGCGCACTTCTGCAACGAGCTCC 510
 3543 ACCGTGAGCTGCGCACTGTGAGCTGCGCGAGCTTGGCGCACTTCTGCAACGAGCTCC 3602
 511 AGGCGCTGCTGGGACAGCTTGGGCGGTCAATGGACCTTGGGCTAACCACTGCCCCAGC 570
 3603 AGGCGCTGCTGGGACAGCTTGGGCGGTCAATGGACCTTGGGCTAACCACTGCCCCAGC 3662
 571 CGCTGCTGGGAGTGAACCACTTGAATCTCTGCGCCCTGCGCCAGATGACTTCTCCAGA 630
 3663 CGCTGCTGGGAGTGAACCACTTGAATCTCTGCGCCCTGCGCCAGATGACTTCTCCAGA 3722
 631 AGATGACGACTTCTGAGCTGCTGAAGAGCTGACAGCTGAGCTGTGGCGCTGGCCAGG 690
 3723 AGATGACGACTTCTGAGCTGCTGAAGAGCTGACAGCTGAGCTGTGGCGCTGGCCAGG 3782
 691 ACTTCAACCGGCTCAAGAGAGATGACAGCTTCAAGAGCTGACAGCTTCAAGAGCTGAG 750
 3783 ACTTCAACCGGCTCAAGAGAGATGACAGCTTCAAGAGCTGACAGCTTCAAGAGCTGAG 3842
 751 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTTCTGCTCCCTCC 795
 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTTCTGCTCCCTCC 3887

RESULT 10
US-09-016-534-3
Sequence 3, Application US/09016534
Patent No. 6143874
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: ELIOTT, GARY S.
APPLICANT: SAMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc.feature
LOCATION: 137..138
OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED"
OTHER INFORMATION: REGION OF >1KB"
US-09-016-534-3
Query Match 65.7%; Score 523.4; DB 3; Length 5087;
Best Local Similarity 99.8%; Pred. No. 16-115; Indels 1; Gaps 0;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 271 ATCTGAACCTGAGGCGCCCTTTCAACAGAGCCAGACTTCAACCTCCCGCTGGGGG 330
DB 3363 AGCTGAACCTGAGGCGCCCTTTCAACAGAGCCAGACTTCAACCTCCCGCTGGGGG 3422
QY 331 CAGAGACTTGCCCGAGGCGCCCTTTGATTTGGAGGTGGGGAAGCTCAATGACAAC 390
DB 3423 CAGAGACTTGCCCGAGGCGCCCTTTGATTTGGAGGTGGGGAAGCTCAATGACAAC 3482
QY 391 TCGGCTGACCCAGAACTAGAGGCGCTTACAGCACTTGTGTTACTTGGCTGGCTCA 450
DB 3483 TCGGCTGACCCAGAACTAGAGGCGCTTACAGCACTTGTGTTACTTGGCTGGCTCA 3542
QY 451 ACCGTGAGGCTGCACTGCTGAGCTGCGCGAGGCTGGCCCACTTCTGCAACAGCTTC 510
DB 3543 ACCGTGAGGCTGCACTGCTGAGCTGCGCGAGGCTGGCCCACTTCTGCAACAGCTTC 3602
QY 511 AAGGCTGCTGGGAGAGCATTTGGGGGCTCATGGAGCTTGGGCTTACCACTGCCCCAGC 570
DB 3603 AAGGCTGCTGGGAGAGCATTTGGGGGCTCATGGAGCTTGGGCTTACCACTGCCCCAGC 3662

QY 571 CGCTGCTGGAGAGTGAACCCACTTGAACCTTGGCCCTGCGCCCAAGTACTTCTCCAGA 630
DB 3663 CGCTGCTGGAGAGTGAACCCACTTGAACCTTGGCCCTGCGCCCAAGTACTTCTCCAGA 3722
QY 631 AGATGAGAGACTTCTGGCTGCTGAAGAGAGCTGAGACCTTGTGGCGCTTGGCCAAAG 690
DB 3723 AGATGAGAGACTTCTGGCTGCTGAAGAGAGCTGAGACCTTGTGGCGCTTGGCCAAAG 3782
QY 691 ACTTCAACCGGCTCAAGAAAGATGAGAGAGCTTCCAGAGCTGACCTACCTCCAGACTGG 750
DB 3783 ACTTCAACCGGCTCAAGAAAGATGAGAGAGCTTCCAGAGCTGACCTACCTCCAGACTGG 3842
QY 751 GGGCTCATGGCTTCTGACTTCTGACTTCTGACTTCTCTCTTGGCTCCCC 795
DB 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTTGGCTCCCC 3887
RESULT 11
US-09-106-182-7
Sequence 7, Application US/09106182
Patent No. 6046035
GENERAL INFORMATION:
APPLICANT: Shi, Yangu
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Cardiotrophin-like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF385
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-106-182-7
Query Match 10.1%; Score 80.2; DB 3; Length 396;
Best Local Similarity 96.5%; Pred. No. 1.9e-10; Indels 3; Gaps 0;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 711 AAGATGAGAGCTTCCAGAGAGTGAACCTTGAACCTTGGGGGCTCATGGCTTGAATT 770
DB 4 AAGATGAGAGCTTCCAGAGAGTGAACCTTGAACCTTGGGGGCTCATGGCTTGAATT 63
QY 771 CTGACCTTCTCTCTTGGCTCCCC 795
DB 64 CTGACCTTCTCTCTTGGCTCCCC 88

RESULT 12

US-09-335-409-1
Sequence 1, Application US/09335409
Patent No. 6121029
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goelach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/335.409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-09-335-409-1

Query Match 5.6%; Score 44.8; DB 3; Length 68750;
Best Local Similarity 50.0%; Pred. No. 0.16;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 456 CAGGCTGCCACTGTGAGTGGCCGACGCTTGACCATTCTGCACGAGCTCCAGAGGC 515
DB 57992 CAGGTAGCGAGTCGGAGAGCCGGGGAGAACGTCCGCCCTTCGGATTCACGCCCGCGGC 58051
QY 516 CTGCTGGGAGCATTTGCGGCGCTCATGGCAGCTCTGGGCTACCACTGCCCGCCGCTG 575
DB 58052 GTGCTGCGCGGATGCGGGCGCTCGAGACCCCGGCAAGGTGCAACTCCGCCCGCTGCGC 58111
QY 576 CTTGGAGCTGAACCCCACTTGAGCTCTGCGCCCTGCCACAGTGAATCTCTCCAGAGATG 635
DB 58112 GCCCGCTTCATGCGCGCGCTGCGCGCTATCTATGCTGCTCGCCGAGATGGGG 58171
QY 636 GACGACTTGTGCTGTGTAAGAGCTGCAGACTGCTGCTGAGCG 679
DB 58172 CTTCAATACGCGCCGCGGCTGCGGGGGCTGCGCGAGCTGTGGCG 58215

RESULT 13

US-09-568-102-1
Sequence 1, Application US/09568102
Patent No. 6346404
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goelach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568.102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335.409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-09-568-102-1

Query Match 5.6%; Score 44.8; DB 4; Length 68750;
Best Local Similarity 50.0%; Pred. No. 0.16;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 456 CAGGCTGCCACTGTGAGTGGCCGACGCTTGACCATTCTGCACGAGCTCCAGAGGC 515
DB 57992 CAGGTAGCGAGTCGGAGAGCCGGGGAGAACGTCCGCCCTTCGGATTCACGCCCGCGGC 58051
QY 516 CTGCTGGGAGCATTTGCGGCGCTCATGGCAGCTCTGGGCTACCACTGCCCGCCGCTG 575
DB 58052 GTGCTGCGCGGATGCGGGCGCTCGAGACCCCGGGAAGGTGCAACTCGCGCCGCTGCGC 58111
QY 576 CTTGGAGCTGAACCCCACTTGAGCTCTGCGCCCTGCCACAGTGAATCTCTCCAGAGATG 635
DB 58112 GCCCGCTTCATGCGCGCGCTGCGCGCTATCTATGCTGCTCGCCGAGATGGGG 58171
QY 636 GACGACTTGTGCTGTGTAAGAGCTGCAGACTGCTGCTGAGCG 679
DB 58172 CTTCAATACGCGCCGCGGCTGCGGGGGCTGCGCGAGCTGTGGCG 58215

RESULT 14

US-09-567-969-1
Sequence 1, Application US/09567969
Patent No. 6355457
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goelach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567.969
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335.409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-09-567-969-1

Query Match 5.6%; Score 44.8; DB 4; Length 68750;
Best Local Similarity 50.0%; Pred. No. 0.16;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 456 CAGGCTGCCACTGTGAGTGGCCGACGCTTGACCATTCTGCACGAGCTCCAGAGGC 515
DB 57992 CAGGTAGCGAGTCGGAGAGCCGGGGAGAACGTCCGCCCTTCGGATTCACGCCCGCGGC 58051
QY 516 CTGCTGGGAGCATTTGCGGCGCTCATGGCAGCTCTGGGCTACCACTGCCCGCCGCTG 575
DB 58052 GTGCTGCGCGGATGCGGGCGCTCGAGACCCCGGGAAGGTGCAACTCGCGCCGCTGCGC 58111
QY 576 CTTGGAGCTGAACCCCACTTGAGCTCTGCGCCCTGCCACAGTGAATCTCTCCAGAGATG 635
DB 58112 GCCCGCTTCATGCGCGCGCTGCGCGCTATCTATGCTGCTCGCCGAGATGGGG 58171
QY 636 GACGACTTGTGCTGTGTAAGAGCTGCAGACTGCTGCTGAGCG 679
DB 58172 CTTCAATACGCGCCGCGGCTGCGGGGGCTGCGCGAGCTGTGGCG 58215

RESULT 15

US-09-568-480-1
Sequence 1, Application US/09568480
Patent No. 6355458
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross

; APPLICANT: Cyr, Devon
 ; APPLICANT: Goerlach, Joern
 ; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
 ; FILE REFERENCE: 4-30582A
 ; CURRENT APPLICATION NUMBER: US/09/568,480
 ; PRIORITY FILING DATE: 2000-05-10
 ; PRIOR APPLICATION NUMBER: 09/335,409
 ; PRIORITY FILING DATE: 1999-06-17
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 1
 ; LENGTH: 68750
 ; TYPE: DNA
 ; ORGANISM: Sorangium cellulosum
 ; US-09-568-480-1

Query Match 5 6%; Score 44.8; DB 4; Length 68750;
 Best Local Similarity 50.0%; Pred. No. 0.16; Indels 0; Gaps 0;
 Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
 QY 456 CAGGCTGCCACTGCTGAGCTGCGCCGACGCTGAGCCCTTCTGACAGAGCTCCAGAGGC 515
 DB 57992 CAGGTAGCGAGTCGGAGCGCGGGGAACTCGCGCCCTTCGGATCCAGCGCCGCGGC 58051
 QY 516 CTGCTGGGAGAGATTGCGGCGCTCATGTGAGCTTGGGCTACCCACTGCCAGCCGCTG 575
 DB 58052 GTGCTGCGCGGATCGGCGCGCTCGAGACCCCGGAGGTGGAACCTCGCGCCGCTGCGC 58111
 QY 576 CCTGGGACTGAACCCACTTGGACTCTGCGCCCTGCGCCACAGAGACTTCTCCAGAGATG 635
 DB 58112 GCCCGGCTTCATGCGCGCGCTGCGCGCTATCTATGTGCGCTGCGCGAGATGGGG 58171
 QY 636 GACGACTTCTGCTGCTGAAGAGCTGACAGACTGCTGAGG 679
 DB 58172 CTTCAATAGCGCCCGCGCTTGGCGGGGCTCGCGAGCTGTGGC 58215

Search completed: February 9, 2004, 06:13:03
 Job time : 78.1015 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 9, 2004, 06:14:57 ; Search time 36 Seconds
(without alignments)
1612.829 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226
Sequence: 1 MDLRAGDSWGLACTIVLM.....KKKMPAAVTLHGANGF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_YEAST:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1226	100.0	225	4 Q9UBD9	Q9UBD9 homo sapien
2	1193	97.3	225	11 Q9QZM3	Q9QZM3 mus musculu
3	150.5	12.3	215	13 Q9PUJ1	Q9PUJ1 plethodon j
4	150.5	12.3	215	13 Q9PUJ0	Q9PUJ0 plethodon j
5	150.5	12.3	215	13 Q9PUJ2	Q9PUJ2 plethodon j
6	148.5	12.1	215	13 Q9PU19	Q9PU19 plethodon j
7	97.5	8.0	318	4 Q9E1S2	Q9E1S2 homo sapien
8	97.5	8.0	530	3 Q8XUE9	Q8XUE9 homo sapien
9	97	7.9	8601	2 Q8GM87	Q8GM87 symbiont ba
10	96.5	7.9	243	4 Q8NEV9	Q8NEV9 homo sapien
11	96.5	7.9	455	11 Q9CMV7	Q9CMV7 mus musculu
12	94	7.7	287	4 Q8N358	Q8N358 homo sapien
13	93	7.6	392	2 Q8KXK2	Q8KXK2 microsomasp
14	92	7.5	332	10 Q9MAU1	Q9MAU1 arabidopsis
15	91.5	7.5	716	16 Q8P199	Q8P199 xanthomonas
16	89.5	7.3	771	2 Q9S309	Q9S309 porphyromon

17	89	7.3	733	16 Q91664	Q91664 pseudomonas
18	88	7.2	392	11 Q8B113	Q8B113 mus musculu
19	88	7.2	422	11 Q8BGR5	Q8BGR5 mus musculu
20	87	7.1	955	11 Q88287	Q88287 mus musculu
21	87	7.1	1561	11 Q88286	Q88286 mus musculu
22	86.5	7.1	379	2 Q8KRX4	Q8KRX4 streptomyce
23	86.5	7.1	640	16 Q54153	Q54153 streptomyce
24	85.5	7.0	522	7 Q8WHM4	Q8WHM4 mus musculu
25	85.5	7.0	1154	11 Q921R2	Q921R2 mus musculu
26	85	6.9	476	11 Q8R363	Q8R363 mus musculu
27	85	6.9	727	11 Q88841	Q88841 mus musculu
28	84.5	6.9	294	11 Q9CPZ1	Q9CPZ1 mus musculu
29	84.5	6.9	389	17 Q9YA71	Q9YA71 aeropyrum p
30	84	6.9	200	16 Q8YB81	Q8YB81 bruceella me
31	84	6.9	232	16 Q8FX31	Q8FX31 bruceella su
32	84	6.9	294	4 Q9NXX5	Q9NXX5 homo sapien
33	84	6.9	411	16 Q9RVF3	Q9RVF3 deinococcus
34	84	6.9	559	16 Q83432	Q83432 treponema p
35	84	6.9	655	11 Q8BY35	Q8BY35 mus musculu
36	84	6.9	876	4 Q9P210	Q9P210 homo sapien
37	83.5	6.8	310	4 Q9S159	Q9S159 homo sapien
38	83.5	6.8	5990	2 Q9RLP6	Q9RLP6 mycobacteri
39	83	6.8	222	2 Q9LS84	Q9LS84 streptococ
40	83	6.8	4782	11 Q8K1G6	Q8K1G6 mus musculu
41	82.5	6.7	310	4 Q9UID0	Q9UID0 homo sapien
42	82.5	6.7	542	16 Q9HTB5	Q9HTB5 pseudomonas
43	82.5	6.7	1122	10 Q8GV08	Q8GV08 oryza sativ
44	82	6.7	283	2 Q9ZB87	Q9ZB87 pseudomonas
45	82	6.7	468	16 Q8DHQ5	Q8DHQ5 synchococ

ALIGNMENTS

RESULT 1

ID	Q9UBD9	PRELIMINARY;	PRT;	225 AA.
AC	Q9UBD9;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Neurotrophin-1/B-cell stimulating factor-3 (Cardiotrophin-like cytokine) (Similar to cardiotrophin-like cytokine, neurotrophin-1/B-cell stimulating factor-3).			
DE	cell stimulating factor-3).			
GN	CLC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9432254; PubMed=10500198;			
RA	Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S., Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Mann F., Simonet W.S., Boone T., Chang M.-S.;			
RA	"Novel neurotrophin-1/B cell-stimulating factor-3: A cytokine of the IL-6 family.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=9938254; PubMed=10448081;			
RA	Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J., Ruben S., Alderson R.F.;			
RA	"Computational EST database analysis identifies a novel member of the neurotrophin-like cytokine family.";			
RT	biochem. Biophys. Res. Commun. 262:132-138(1999).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RA	Hu X., Xu Y., Zhang B., Peng X., Yuan J., Qiang B.;			
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Kidney;			

RA Strausberg R.;
 Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF176912; AAF00992.1; -
 DR EMBL; AF172854; AAD54284.1; -
 DR EMBL; AF176911; AAF00991.1; -
 DR EMBL; AY049779; AAL15436.1; -
 DR EMBL; BC012939; AAL12939.1; -
 SQ SEQUENCE 225 AA; 25176 MW; E2DD4B6280833B55 CRC64;

Query Match 100.0%; Score 1226; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.7e-106; Indels 0; Gaps 0;
 Matches 225; Conservative 0; Mismatches 0;

QY 1 MDLRAGDSWGMKLACTVYLMHLPAVPALNRTGDPGPGPSIQTYDLTRYLHQLSLAGT 60
 DB 1 MDLRAGDSWGMKLACTVYLMHLPAVPALNRTGDPGPGPSIQTYDLTRYLHQLSLAGT 60
 QY 61 YLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWWSLNDKRLTONYEAYSHLCLYRGL 120
 DB 61 YLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWWSLNDKRLTONYEAYSHLCLYRGL 120
 QY 121 NROAATAEIRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPGPAHSDFLQ 180
 DB 121 NROAATAEIRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPGPAHSDFLQ 180
 QY 181 KMDDFWMLKELOTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225
 DB 181 KMDDFWMLKELOTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225

RESULT 2

QOQZM3 PRELIMINARY; PRT; 225 AA.

AC Q9QZM3; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Neurotrophin-1/B-cell stimulating factor-3.
 GN BSF3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99432254; PubMed=10500198;
 RA Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,
 RA Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Mann F.,
 RA Simonet W.S., Boone T., Chang M.-S.;
 RT "Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
 RT IL-6 family."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).
 DR EMBL; AF176913; AAF00993.1; -
 DR MGI; MGI:1930088; BSF3.
 SQ SEQUENCE 225 AA; 25261 MW; 68B1FEAAB7F1A950 CRC64;

Query Match 97.3%; Score 1193; DB 11; Length 225;
 Best Local Similarity 96.9%; Pred. No. 5e-105; Indels 0; Gaps 0;
 Matches 218; Conservative 3; Mismatches 4;

QY 1 MDLRAGDSWGMKLACTVYLMHLPAVPALNRTGDPGPGPSIQTYDLTRYLHQLSLAGT 60
 DB 1 MDLRAGDSWGMKLACTVYLMHLPAVPALNRTGDPGPGPSIQTYDLTRYLHQLSLAGT 60
 QY 61 YLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWWSLNDKRLTONYEAYSHLCLYRGL 120
 DB 61 YLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWWSLNDKRLTONYEAYSHLCLYRGL 120
 QY 121 NROAATAEIRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPGPAHSDFLQ 180
 DB 121 NROAATAEIRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPGPAHSDFLQ 180
 QY 181 KMDDFWMLKELOTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225
 DB 181 KMDDFWMLKELOTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225

DB 181 KMDDFWMLKELOTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225

RESULT 3

Q9PUJ1 PRELIMINARY; PRT; 215 AA.

ID Q9PUJ1; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Receptivity factor isoform 2 precursor.
 GN PRF.
 OS Plethodon jordanii (Salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroides; Plethodontidae;
 OC Plethodon.
 OX NCBI_TaxID=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99420364; PubMed=10489368;
 RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial
 RT salamander."
 RT Science 285:1907-1909(1999).
 DR EMBL; AF181481; AAF01026.1; -
 KM Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 215 AA; 24080 MW; B341BBB74E28438 CRC64;

Query Match 12.3%; Score 150.5; DB 13; Length 215;
 Best Local Similarity 26.2%; Pred. No. 3e-06; Indels 7; Gaps 3;
 Matches 42; Conservative 31; Mismatches 80;

QY 56 SLAGTYLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWWSLNDKRLTONYEAYSHLCL 115
 DB 55 SLPLTYLNFQGAPLSDPPYOLPHIVANLPTRAMDYDFEMKQTBETRLNNMLYFYSAIVE 114
 QY 116 YLR-GLNRQ---AATAELRRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPG 170
 DB 115 FLKEMTQEDLNPELSLKKAFEEAMANSNTLSKISDITQMSVTTILP--KPLVV 172
 QY 171 PGPAHSDFLQKMDDFWMLKELOTWLMRSKDFNRLKKKQ 210
 DB 173 PPGSAYFRKKLRGSGVCKEYKERVLTFRDFEFLAKKYQ 212

RESULT 4

Q9PUJ0 PRELIMINARY; PRT; 215 AA.

ID Q9PUJ0; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Receptivity factor isoform 3 precursor.
 GN PRF.
 OS Plethodon jordanii (Salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroides; Plethodontidae;
 OC Plethodon.
 OX NCBI_TaxID=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99420364; PubMed=10489368;
 RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial
 RT salamander."
 RT Science 285:1907-1909(1999).
 DR EMBL; AF181482; AAF01027.1; -
 KM Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 215 AA; 24024 MW; 6EB6E64AD93A1343 CRC64;

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Query Match          12.3%; Score 150.5; DB 13; Length 215;
Best Local Similarity 27.1%; Pred. No. 3e-06;
Matches 45; Conservative 34; Mismatches 72; Indels 15; Gaps 4;

QY 56 SLAGTYLNTLGPFPNPPDNPRLGAEITLPRATVDLEWRSINDKRLTONTYEAYSHLIC 115
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 55 SLPTLYLSFOGAPLSDPDYQLPHIKVNLPTAAMDYDFIRQDETRLNKNLYFYSAIVE 114
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 116 YLR-----GLN--RQAATAEIRSLAHFCTSLQGLSIGVMAALGYPLPQPLPGTVE 166
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 115 FLKEAMTEQBDLNPALSLKAKFEEMANSNTLISKISDITMGMSVTITLP--K 168
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 167 PWTGPASDPLQKMDPFLKELQTLWLRSAKDNPRLKXKQPP 212
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 169 PLVVPKGSAYPESKLRGVCVEYKERVFLTKRDMFLAEKXQGP 214
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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RESULT 5
Q9PUJ2 PRELIMINARY; PRT; 215 AA.
AC Q9PUJ2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE Receptivity factor isoform 1 precursor.
GN PRF.
OS Plethodon jordani (Salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
OC Plethodon.
OC NCBI_TaxID=8336;
RN (1)
RP MEDLINE=99420364; PubMed=10489368;
RA Rollman S.M., Houck L.D., Feldhoff R.C.;
RT "Proteinaceous pheromone affecting female receptivity in a terrestrial
RT salamander.";
RL Science 285:1907-1909(1999).
DR EMBL; AF181480; AAF01025.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 215 AA; 24138 MW; B1906BB66335738 CRC64;

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Query Match          12.3%; Score 150.5; DB 13; Length 215;
Best Local Similarity 26.2%; Pred. No. 3e-06;
Matches 42; Conservative 31; Mismatches 80; Indels 7; Gaps 3;

QY 56 SLAGTYLNTLGPFPNPPDNPRLGAEITLPRATVDLEWRSINDKRLTONTYEAYSHLIC 115
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 55 SLPTLYLSFOGAPLSDPDYQLPHIKVNLPTAAMDYDFIRQDETRLNKNLYFYSAIVE 114
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 116 YLR-----AATAEIRSLAHFCTSLQGLSIGVMAALGYPLPQPLPGTVEPTWT 170
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 115 FLKEAMTEQBDLNPALSLKAKFEEMANSNTLISKISDITMGMSVTITLP--KPLV 172
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 171 PGPASDPLQKMDPFLKELQTLWLRSAKDNPRLKXKQ 210
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 173 PEGSAVFRKQLRGVVCVEYKERVLLTKRDFEFLAKXQ 212
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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RESULT 6
Q9PUJ9 PRELIMINARY; PRT; 215 AA.
AC Q9PUJ9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE Receptivity factor isoform 4 precursor.
GN PRF.
OS Plethodon jordani (Salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
OC Plethodon.

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OX NCBI_TaxID=8336;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99420364; PubMed=10489368;
RA Rollman S.M., Houck L.D., Feldhoff R.C.;
RT "Proteinaceous pheromone affecting female receptivity in a terrestrial
RT salamander.";
RL Science 285:1907-1909(1999).
DR EMBL; AF181483; AAF01028.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 215 AA; 24054 MW; A4A412135FFA4E7F CRC64;

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Query Match          12.1%; Score 148.5; DB 13; Length 215;
Best Local Similarity 25.9%; Pred. No. 4.6e-06;
Matches 42; Conservative 33; Mismatches 80; Indels 7; Gaps 3;

QY 56 SLAGTYLNTLGPFPNPPDNPRLGAEITLPRATVDLEWRSINDKRLTONTYEAYSHLIC 115
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 55 SLPTLYLSFOGAPLSDPDYRLPHIKVNLPTAAMDYDFIRQDETRLNKNLYFYSAIVE 114
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 116 YLR-----AATAEIRSLAHFCTSLQGLSIGVMAALGYPLPQPLPGTVEPTWT 170
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 115 FLKEAMTEQBDLNPALSLKAKFEEMANSNTLISKISDITMGMSVTITLP--KPLV 172
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 171 PGPASDPLQKMDPFLKELQTLWLRSAKDNPRLKXKQPP 212
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 173 PFGSAVFRKQLRGVVCVEYKERVFLTKRDMFLAEKXQGP 214
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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RESULT 7
Q9ELS2 PRELIMINARY; PRT; 318 AA.
AC Q9ELS2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein FLJ25132.
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Nakagawa K., Mizuno S., Morinaga M., Suzuki Y., Hata H.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RT "NEO human cDNA sequencing project.";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK057861; BAB71598.1; -.
KW Hypothetical protein.
SQ SEQUENCE 318 AA; 34305 MW; 62E5CFB1A5998F40 CRC64;

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Query Match          8.0%; Score 97.5; DB 4; Length 318;
Best Local Similarity 25.1%; Pred. No. 0.53;
Matches 49; Conservative 19; Mismatches 76; Indels 51; Gaps 9;

QY 6 GDSWGMCLCTCYVHLPAVPAALNRTG---DGPSPSIOKTYDLPRLYEHQURSLAGTYL 62
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 82 GTECSFLYLYSEVEHFCPLPFRNQTAAQAPKPPKQAVF-----RSLYSHLL 131
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 63 NYLGPFPNPPDNPRLGAEITL-----PRATVDLEWV-----RSLNDKRLTONTYEAYS 111
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 132 DLMGS-----GKESLIFMKKRTKTLAQ---WALAAGLAKGATGQDQ--K 174
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 112 HLLCTLRGLNROAATAEIRSLAHFCTSLQGLSIGVMA-----ALG-----YPLPQ 161
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 175 QLVHIGFLTESGVFSFPRVLMFLCSALAMASALAPALATLTALGRALCRIPAPNP 234
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 162 LPGEPTWTPGPAS 176
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Db 235 LPSRSTPSTPYES 249

RESULT 8

Q8X0E9 PRELIMINARY; PRT; 530 AA.
 AC Q8X0E9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hypothetical 59.4 kDa protein.
 GN B14a6.080.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OK NCBI_Taxid=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohnsels J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL670007; CAD21310.1; -
 DR InterPro; IPR001810; F-box.
 DR PROSITE; PS50181; FBOX; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 530 AA; 59352 MW; 70382EB15F71BB9D CRC64;

Query Match 8.0%; Score 97.5; DB 3; Length 530;
 Best Local Similarity 24.8%; Pred. No. 1;
 Matches 41; Conservative 22; Mismatches 65; Indels 37; Gaps 6;
 QY 64 YLGPPEPNEPFPRLGAEITLPPRA-TVDELVRSINDKRLTONYEAVSHLCYLRGLNR 122
 DB 236 FLVPPYLPEDFLPYLAGLKKHLVLDADLATRHDEIQYLKKFLALTPNLTWLR----- 291
 QY 123 QAAITELRLSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPPT-----EPTWTPGP 173
 DB 292 ----VNFERSISHY-----GKKEALLKWLASSLRPGTWSGGLINADPSRLPP 336
 QY 174 AHSDELQKMDFWLKELOTWLRSAKDFNRLLKKXQPPAAAVTL 218
 DB 337 VEPDHEQD---IGQLDV---SANTLYRLFNKFSSTLKATSL 373

RESULT 9

Q8GM87 PRELIMINARY; PRT; 8601 AA.
 AC Q8GM87;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Mixed type I polyketide synthase/nonribosomal peptide synthetase.
 GN PEDP.
 OS symbiont bacterium of Paederus fuscipes.
 OC Bacteria.
 OK NCBI_Taxid=176282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22294974; PubMed=12381784;
 RA Piel J.;
 RT "A polyketide synthase-peptide synthetase gene cluster from an
 RT uncultured bacterium of Paederus beetles";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).
 DR EMBL; AY059471; AAL27851.1;
 SQ SEQUENCE 8601 AA; 948046 MW; C498ACB80B5082C7 CRC64;

Query Match 7.9%; Score 97; DB 2; Length 8601;
 Best Local Similarity 25.6%; Pred. No. 43;

Matches 51; Conservative 37; Mismatches 69; Indels 42; Gaps 12;

QY 58 AGTYINLYGPPNEPFPRLGAEITLPPRA-TVDELVRSINDKRLTONYEAVSHLCYLR 117
 DB 5078 SGTNVLVVEEFVRSNSDPRLVDVSSSTAQPEL-TILSTYDAERLS---EVLNLAHFV 5133
 QY 118 RGLNRQAATAELRLSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPPT 166
 DB 5134 RQAQNPADLE-RSLADLATLQTRGRAMBQRYVALVGDLAGLLEALS-ALREERPCPV 5191
 QY 167 PWT-----PGPAH-----SDPLQKMDDFL-----LKEI-QTWLMSADFNRLK 206
 DB 5192 SVWSGRVPEPGRGAEITVADQPAELLQRIPO-WIARGADELIAQAVVAGAPIDWCQR 5250
 QY 207 KMKQPPAAAVTLHLGANGF 225
 DB 5251 KR-RPPR--RVHLPSYFP 5265

RESULT 10

Q8NEV9 PRELIMINARY; PRT; 243 AA.
 AC Q8NEV9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE IL-27 p28 subunit.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OK NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfanz S., Timans J., Cheung J., Rosales R., Kanzler H., Gilbert J.,
 RA Hibbert L., Churakova T., Travis M., Vatsberg E., Blumenschein W.,
 RA Matsson J., Wagner J., To W., Zurawski S., McClanahan T., Gorman D.,
 RA Bazan F., de Waal Malefyt R., Renwick D., Kaselahn R.;
 RT "IL-27 p28 subunit sequences";
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY099296; AAM34498.1; -
 SQ SEQUENCE 243 AA; 27476 MW; 2FA8ABEB6C6F1AEB CRC64;

Query Match 7.9%; Score 96.5; DB 4; Length 243;
 Best Local Similarity 23.7%; Pred. No. 0.46;
 Matches 58; Conservative 26; Mismatches 104; Indels 57; Gaps 9;

QY 1 MDLRAGD-SWGMALCLCTVL-----WHLPAVPAALNRTGDPGPGSIQK-----TYDL 46
 DB 1 MGQTAGDGLGMRSLSLPLPLLVQAGVWGFPRRPG-----RPQISLQELRRREFVSLHL 53
 QY 47 TRYLEHQRLSLAGTYLN-----YLGPPEPNEPFPRLGAEITLPPRA-TVDELVRSIN 98
 DB 54 ARKLSEVRGQAHFRAESHLPGVNLVLLP-----LG-RQLPVSSTLPQAWRLS 101
 QY 99 DKLRLTQYEAVSHLCYLRGLNRQAATAELRL-SLAHFTCTSLQGLGSIAGVMAALGYP 157
 DB 102 DPERLCFTSLTLPQPHAPLGSIGQGRWTKERNQMLAMRLDLKDQHLHAFQYLAAGFN 161
 QY 158 LPQP-----LPGETPTWTPGPAHSDFLQKMDFWLKELOTWLRSAKDF 202
 DB 162 LPPEEEEEEDEEBERKGLPLGALGSLAQGPAQVSWPQLSTYRLHLSLELVLSAVAL 221
 QY 203 NRLKK 207
 DB 222 LILSK 226

RESULT 11

Q9CWV7 PRELIMINARY; PRT; 455 AA.
 AC Q9CWV7;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE 2410003H12RIK protein.
 GN 2410003H12RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Azawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kodera K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Perole G., Quackenbush J.,
 RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Maehio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
 RA Blake J., Beffelli D., Bojunga N., Carlini P., de Bonaldo M.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK010358; BAB26878.1; -;
 DR MGD; MGI:1919221; 2410003H12RIK.
 SQ SEQUENCE 455 AA; 51481 MW; 201868B814EB9CF6 CRC64;

Query Match 7.9%; Score 96.5; DB 11; Length 455;
 Best Local Similarity 22.4%; Pred. No. 1;
 Matches 59; Conservative 24; Mismatches 89; Indels 91; Gaps 12;

QY 7 DSGMGLACTCTVLM-HLPAVPALNRGDPG-----FGPSIQTYDITRYLEHQLMS 56
 DB 29 DARNYOSCFWQDFAHFEPEVFLHRTYPRGKVLTYFLVDGPRVQVEGFLARAV----- 82
 QY 57 LAGTYLVLYGPPFNE-----PDENPRPLGAEFLPRATVDLEWRSINDKRLRL 104
 DB 83 -----YFAIPFNEDARGLAQMFQVFKFNP-----AMERVNITL--- 116
 QY 105 QNVEAVSHLTCYLRGLNRQAATAELRSLSAHFCTSLQGLGSIAGVMAALGYPLQP 161
 DB 117 ----VDPHFL-LPFTLMEFPFTLEVLISAFHICKFLQGRKYL-----PLGQPVQR 162
 QY 162 ----LPGEPFTPTPCPAH-----SDPLQKMDFWLKEIQTWI--WRSADKF 202
 DB 163 LLLSSLSQSTGATAGATRLKLYTLNLCIPSSRLPELHSHMLND-RIMVLHWRSRAS 221
 QY 203 NRLKKMGQPPAAVATLHLGANGF 225
 DB 222 SKYFOSLEIWAHILSOPFGTTPF 244

RESULT 12
 OGN358 PRELIMINARY; PRT; 287 AA.
 AC OGN358;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC Tissue=Blood;
 RA Strausberg R.;
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC028076; AAH28076.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 287 AA; 32156 MW; 6E571ECA0328E74E CRC64;

Query Match 7.7%; Score 94; DB 4; Length 287;
 Best Local Similarity 22.3%; Pred. No. 0.99;
 Matches 47; Conservative 18; Mismatches 62; Indels 84; Gaps 9;

QY 15 LCTVLMHLPAVPALNRGDPGSPSIQTYD-----LTRY---LEHQL--RSLAG 59
 DB 132 LRPVWLRF-----PDGPTLNTLQCPGSRQSPGVLRFRNQMLHVLTGAFIN 181
 QY 60 TLYLVY---LGPFPNEPDENPRPLGAEFLPRATVDLEWRSINDKRLRLTONYEAVAL 115
 DB 182 TYLFYGAAYVGP-----ESSSVYSIRLA 204
 QY 116 YLRGLNRQAATAELRSLSAHFCTSLQGLGSI-----GVMAALGYPLQPLPTEPTW 169
 DB 205 YL-----LSPLACLLLCFCGTLHQLSTLASGPGAGPWAHPACPLPGPLRLQ 256
 QY 170 TEGPAHSDPLQKM-----DDFWLKEIQTWLM 196
 DB 257 LRPPIHAQVLRAGAMGSDTWGRSGFLPWGW 287

RESULT 13

O8KNF2 PRELIMINARY; PRT; 392 AA.
 AC O8KNF2;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Calg.
 GN CALG.
 OS Micromonospora echinospora (Micromonospora purpurea).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micromonosporinae; Micromonosporaceae; Micromonospora.
 ON NCBI_TaxID=1877;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRL 15839;
 RA Ahlert J., Shepard E., Lomovskaya N., Zazopoulos E., Staffa A.,
 RA Bachmann B.O., Huang K., Fomstein L., Cziorny A., Whitwam R.E.,
 RA Farnet C.M., Thorson J.S.;
 RT "The calicheamicin gene cluster and its iterative type I PKS."
 RL Science 0-0(2002).
 DR EMBL; AF497482; AAM70336.1; -;
 DR InterPro; IPRO00890; Acetate_kin.
 DR PROSITE; PS01076; ACETATE_KINASE 2; 1.
 SQ SEQUENCE 392 AA; 41151 MW; 8D298611281E065E CRC64;

Query Match 7.6%; Score 93; DB 2; Length 392;
 Best Local Similarity 26.4%; Pred. No. 1.9;
 Matches 43; Conservative 15; Mismatches 61; Indels 44; Gaps 7;

QY 45 DITRYLEHQLRSLA-----GTLYLVLYGPPFNEPDENPRPLGAEFLPR 86
 DB 146 DITRSIEEYVRGLAQRLGIDLPGRIDGNGNFIDIFPSLOEPFRARPRHRLRPVVF 205
 QY 87 ATV-DLEWRSINDKRLRLTONYEAVALSHLLCYLRGLNRQAATAELRSLSAHFCTSLQGLG 145
 DB 206 AAGQGLPAVLSSRDYAR-----PLVYVTLTGSSGTEYVLR-----AIDGLAG 249
 QY 146 SIAGVMAALGYPLQPLPTEP-----TWTGPA---HSDPL 179
 DB 250 LDADVLVASGSLDVSGLGEVPAVNLRSWVQALLPRVDLV 292

RESULT 14

Q9MAU1 PRELIMINARY; PRT; 332 AA.
 AC Q9MAU1: 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE F13M7.8 protein (Hypothetical protein).
 GN F13M7.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 OK NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. columbiana;
 RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Liu, S.,
 Li J., Kremenetskaia I., Luros J., Araujo R., Au M., Bredel V.,
 Buehler E., Conway A., Dewar K., Feng J., Kim C., Kurtz D., Li Y.,
 Palm C., Shinn P., Sun H., Davis R., Ecker J., Federspiel N.,
 RA Theologis A.;
 RT "The sequence of BAC F13M7 from Arabidopsis thaliana chromosome 1.",
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. columbiana;
 RA Theologis A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC004809; AAF4044.1; -;
 DR EMBL; AY085490; AAM62716.1; -;
 DR InterPro; IPR002965; P rich extenan.
 DR PRINTS; PR01217; PRICHEXTENSN.
 KW Hypothetical protein.
 SO SEQUENCE 332 AA; 36793 MW; 18E867141A070F4 CRC64;
 Query Match 7.5%; Score 92; DB 10; Length 332;
 Best Local Similarity 26.4%; Pred. No. 1.9;
 Matches 58; Conservative 24; Mismatches 72; Indels 66; Gaps 13;
 QY 23 PAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLVN----- 64
 DB 113 PSVAGNLSGYV-PRPSF--TYDPGPYEQWESLQOIFIRBNPQIRPLRLGLGSPVG 169
 QY 65 LGPPNEPDPFPPRGATFLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLGLNQA 124
 DB 170 LGPIRASQFLQPRVAP--PTSIID---TSRNKKA-----SKGALAVVRG--RKV 215
 QY 125 ATAELRSL-----AHFCTSLQGLSLGVAALGYPLPPLP--GTEPTWT 170
 DB 216 RITGSSSLVLSLGNKNGAHV-----GIQPRSGIMK-----PLPKPLPVDLTTEISVP 266
 QY 171 PGPAHSDFLQKMDFFWLKELQTLWRSAXDPNRLKTKMQ 210
 DB 267 DDPDESADKDEKDEAVKQL-----SEKDL--LKRHIE 298

RESULT 15
 ID Q8P199 PRELIMINARY; PRT; 716 AA.
 AC Q8P199;
 Q8P199;
 Q8P199;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Peptidase.
 GN XAC2999.
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OC NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cammaran F., Cardozo J., Chabedogo F., Clapina L.P.,
 RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locall E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).
 DR EMBL; AE011942; AAM37844.1; -;
 DR InterPro; IPR006025; Zn_MTPeptidse.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Complete proteome.
 SO SEQUENCE 716 AA; 79145 MW; 0C6D1875E07DDCD CRC64;
 Query Match 7.5%; Score 91.5; DB 16; Length 716;
 Best Local Similarity 25.7%; Pred. No. 5.6;
 Matches 54; Conservative 18; Mismatches 63; Indels 75; Gaps 13;
 QY 22 LPAVPALNRTGDPGPGPSI---QKTYDLTRYLEHQLRSLAG---TYLVNLYGPPNEPDPF 74
 DB 101 LPDAPNAYRSSGVPGAFWGNRADYDLSASIDPATHTLSGEAAITTNH-----SPD 153
 QY 75 NPPLRGATFLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLGLNR-----QAATA 127
 DB 154 -----TLDV-LW-----LQDQNIYRVNARAASRPLRKKEFTDGMQIASV 193
 QY 128 EL-----RRSLAHFCTSLQGLSLGVAALGYPLPPLP-----TEP-TW 169
 DB 194 EIDQGRGROSHAFIVD-----DTRNRVDLPPLAGQKALTVHIRYRTITIGTW 242
 QY 170 TPGPASDFLQKMDFFWLKELQTLWRSAXDPNRLKTKMQ 199
 DB 243 GGRTAVS--ASKQGDIV---EIAQWYPRMA 267

Search completed: February 9, 2004, 06:19:05
 Job time : 41 secs

Db	605	CGTGGCCCTGGCCCAAGTAGCTTCTCTCAGAAATGATATGACTTCTTGCGCTGTGAAGAG	664
Oy	660	CTGCAGACTCTGGCTGTGGGGCTCGGCCAAGACTTCAACCGGCTCAAGAAAGATGCAG	719
Db	665	CTGCAGACCTGGCTATGGGGCTTGACGCCAAGGACTTCAACCGGCTTAAGAAGAATGCAG	724
Oy	720	CCCTCCAGCAGCTGCATCAACCCCTGGACACTGGGGGGCTCATGGCTTTCGACTTTCGACCTT	778
Db	725	CTTCAGACAGCTTCACTCAACCTGCACCTTGAAGGACAATGGTTTCTGACCTCTGACCT	783
RESULT 13			
AAA39483			
ID	AAA39483	standard; cDNA; 819 BP.	
AC	AAA39483;		
XX	24-AUG-2000	(first entry)	
XX			
DE	Murine NNT-1 cDNA.		
XX			
KW	NNT-1; neurotrophic factor; neurotrophic; neuroprotective; treatment;		
KW	anticomulsant; antiparkinsonian; antidiabetic; ophthalmological;		
KW	nervous system degeneration; Alzheimer's disease; Parkinson's disease;		
KW	amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine;		
KW	Huntington's disease; peripheral neuropathy; neural retina degeneration;		
XX	retinopathy; immune disorder; hematopoietic disorder; ss.		
XX			
OS	Mus sp.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	95..772	
FT		/*tag= a	
FT		/product= "NNT-1"	
PN	US6054294-A.		
XX			
PD	25-APR-2000.		
XX			
PF	12-DEC-1997;	97US-0988819.	
XX			
PR	03-FEB-1997;	97US-0792019.	
XX			
PA	(AMGE-) AMGEN INC.		
XX			
PI	Chang M;		
XX			
DR	WPI: 2000-338492/29.		
XX			
DR	P-P8DB; AAY87814.		
XX			
PT	New nucleic acids encoding neurotrophic factors useful for stimulating		
PT	growth of motor or sympathetic neurons for treating neuron cell damage		
PT	-		
XX			
PS	Claim 2a; Fig 4; 42pb; English.		
XX			
CC	This invention describes a novel nucleic acid molecule (I) encoding a		
CC	novel neurotrophic factor (NNT-1) (II) which has neurotrophic,		
CC	neuroprotective, anticomulsant, antiparkinsonian, antidiabetic and		
CC	ophthalmological activity. (II) is useful for producing NNT-1		
CC	polypeptides which are useful for treating patients in whom various		
CC	cells of the central, autonomic, or peripheral nervous system have		
CC	degenerated and/or have been damaged by congenital disease, trauma,		
CC	mechanical damage, surgery, stroke, ischemia, infection, metabolic		
CC	disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1		
CC	proteins are used to treat diseases like Alzheimer's, Parkinson's,		
CC	amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's		
CC	disease, peripheral neuropathy induced by diabetes or other metabolic		
CC	disorders, and/or dystrophies or degeneration of the neural retina such		
CC	as retinitis pigmentosa, drug-induced retinopathies, stationary forms of		
CC	night blindness, progressive cone-rod degeneration, immune disorders and		
CC	hematopoietic disorders. (I) is effective in treating neurological		

CC conditions and promotes neuron regeneration. Neural functions are
CC effectively restored in patients suffering from various neurological
CC disorders. This sequence encodes the murine NMT-1 protein described in
CC the method of the invention.

Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;

Query Match	84.0%	Score 669.4	DB 21	Length 819
Best Local Similarity	92.0%	Pred. No. 6	2e-147	
Matches 717	Conservative 0	Mismatches 61	Indels 1	Gaps 1

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Db	5	ATTAAAGCTTCGCGGAGCGCGAGCTCGGCTCCCACTCGGCAAGAG	64
QY	61	CCGCACTCCGCGCGCCAG - CCGCACTCCGCAAGCTTCGAGCGAGGACTCGGAGG	11
Db	65	CCGCGCCCGCGCCCGGCCCCAGCCCCCATGGAATCTCGAGCGAGGAGCTCGGAGG	12
QY	120	ATGTAGCGTCTGTGCAAGTGTCTGTGGACTTCCTCGCAGTGCAGCTTCAATGCC	17
Db	125	ATGTAGCTTGCCTTAAGCAAGGTGTGTGGCACTCCCTGCAGTGCAGCTTCAATGCC	18
QY	180	ACAGGGGAGCCAGAGGCTGCGCCCTCATCCAGAAAACCTAAGACTCAACCGGCTAACCG	23
Db	185	ACAGGAGATCAGAGGCTGCGCCCTCATCCAGAAAACCTAAGACTCAACCGGCTAACCG	24
QY	240	GAGCAGCAACTCGCAGCTTGTGCGAGCTTAATCTGAATACCTGAGGCCCTTTCAC	29
Db	245	GAGATCAACTCGCAGCTTGTGCGAGCTTAATCTGAATACCTGAGGCCCTTTCAC	30
QY	300	GAGCAGACTTCAACCTTCCCGGCTGGGGGCAAGACTTGCACAGGAGCCACTGTGAC	35
Db	305	GAGCCTGACTCAATCTTCTGAGCTGGGGGCAAGAACTTGCACAGGAGCCACTGTGAC	36
QY	360	TTGAGAGTGTGGAGAGCTCAATGACAAACCTGGGCTGACCCCAAGATACGAGGCTTAC	41
Db	365	TTGAGAGTGTGGAGAGCTCAATGACAGGCTGGGCTGACCCCAAGATACGAGGCTTAC	42
QY	420	AGCAGCTTCTGTACTTGTGCGTGGCTCAACCGTCAAGCTGCACCTGAGCTGAGCTGAGC	47
Db	425	AGTCACTCTGTACTTGTGCGTGGCTCAACCGTCAAGCTGCACAGCTGAGCTGAGC	48
QY	480	CGAGCTTGGCCCACTTCTGCAACAGCTCCAGGCTCTGCTGGGAGCAATTTGGGGCTC	53
Db	485	CGTAGCTTGGCCCACTTCTGTAACAGCTCCAGGCTCTGCTGGGAGCAATTTGGGGCTC	54
QY	540	ATGGCAGCTCTGGGCTAACCACTGGCCCGAGCCGCTGCTGGGACTGAACCCACTTGAAT	59
Db	545	ATGGCAGCTTGGGCTAACCACTGGCCCGAGCTTGGCAGGAGCTGAACCCAGCTTGGGCTC	60
QY	600	CTTGGCCCTGGCCCAAGTACTTCTCCAGAAAGATGAGCGAATTTGGCTGTGAAGAG	65
Db	605	CTTGGCCCTGGCCCAAGTACTTCTCCAGAAAGATGAGCTTCTGGCTGTGAAGAG	66
QY	660	CTGCAAGCTTGTGTGGCTCGGCTCGGCAAGACTTCAACCGGCTCAAGAAAGATGAG	71
Db	665	CTGCAAGCTTGTGTGGCTCGGCTCGGCAAGACTTCAACCGGCTCAAGAAAGATGAG	72
QY	720	CTTCCAGCAGCTGCAATCACTCTGCAACTGGGGGCTAATGCTTTGACTTCTGACTTT	778
Db	725	CTTCCAGCAGCTTCAATCACTCTGCAACTGGGGGCTAATGCTTTGACTTCTGACTTT	783

```

RESULT 14
ABK11649
ID ABK11649 standard; cDNA; 819 BP.
AC ABK11649;
XX
XX
DT 05-JUN-2002 (first entry)
XX
EX Mouse cDNA encoding novel neurotrophic factor NNT1

```

XX Mouse; ss; gene: NNT1; neurotrophic factor; IGF-related disease;
 KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
 KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
 KW vascular reestenosis; rheumatoid arthritis; psoriatic arthritis;
 KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
 KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
 KW inflammatory bowel disease; transplant rejection; reproductive disorder;
 KW graft versus host disease; infertility; miscarriage; preterm labour.
 XX Mus sp.
 XX Location/Qualifiers
 FH Key 95..772
 FT CDS /tag= a
 FT /product= "NNT1"
 FT
 PN MO200215977-A2.
 XX
 XX 28-FEB-2002.
 XX
 PF 17-AUG-2001; 2001MO-US25906.
 XX
 XX 18-AUG-2000; 2000US-226436P.
 PR 16-AUG-2001; 2001US-0931704.
 XX
 XX (AMGE-) AMGEN INC.
 XX Senaldi G;
 PI
 XX MPI; 2002-280867/32.
 DR P-PSDB; AUN08177.
 XX
 PT Treating Immunoglobulin E-related disease, modulating IGE levels in a
 PT patient, preventing IGE-related disease and treating allergic diseases,
 PT involves administering NNT-1 inhibitor to a patient
 XX
 PS Claim 2; Fig 4; 63pp; English.
 CC The invention relates to treating Immunoglobulin E (IGE)-related disease,
 CC modulating IGE levels in a patient, preventing an IGE-related disease,
 CC and treating allergic diseases, comprising administering a
 CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
 CC inhibitor to a patient. Also included are a method of diagnosing an
 CC IGE-related disease or susceptibility to an IGE-related disease, by
 CC determining the presence or amount of expression of an NNT1 polypeptide
 CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
 CC occurring variant, and diagnosing an IGE-related disease or
 CC susceptibility of an IGE-related disease based on the presence or amount
 CC of expression of the polypeptide and a pharmaceutical composition for use
 CC in treating IGE-related disease, comprising the NNT1 inhibitor.
 CC The NNT1 inhibitor is useful for preventing and treating IGE-related
 CC disease, modulating IGE levels, and treating allergic diseases e.g.
 CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,
 CC pollinosis, asthma, immune diseases and disorders, diseases involving
 CC abnormal cell proliferation including cancer, arteriosclerosis and
 CC vascular reestenosis, diseases and conditions relating to dysfunction of
 CC immune system including rheumatoid arthritis, psoriatic arthritis,
 CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,
 CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
 CC bowel disease, transplant rejection, and graft versus host disease, and
 CC reproductive diseases and disorders including infertility, miscarriage,
 CC preterm labour and delivery, and endometriosis. The present sequence
 CC encodes mouse NNT1.
 CC
 XX Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;
 SQ
 Query Match 84.0%; Score 669.4; DB 24; Length 819;
 Best Local Similarity 92.0%; Pred. No. 6.2e-147;
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
 QY 1 ATTAAGCTTCGCGGAGCGCGGCTGCGCTCCCACTCGCGGAGCGAGGAGG 60
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Db 5 ATTAAGCTTCGCGGAGCGCGGCTGCGCTCCCACTCGCGGAGCGAGGAGG 64
 QY 61 CCGGACCCGCGCGGCGGAG-CCCGAGCCCGCANTGACCTCCGAGCGAGGGAGCTCGGGGG 119
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 65 CCGCGCCCGCGCGGCGCGGCGCGCCCGCCGACCTCCGAGCGAGGGAGCTCGGGGGG 124
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 QY 120 ATGTAGAGGTGCTGTGACGGGTGTCTGAGCACTCCCTGAGTCCAGCTCTCAATGCG 179
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 Db 125 ATGTAGCTGTGCTATGACAGGATGCTGTGAGCACTCCCTGAGTCCAGCTTTAATGCG 184
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 QY 180 ACAGGGGAGCCAGGCGCTGCGCCCTCATCCAGAAACCTATGACCTGACCCGCTACCTG 239
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 Db 185 ACAGGAGATCCAGGCGCTGCGCCCTCATCCAGAAACCTATGACCTGACCCGCTACCTG 244
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 QY 240 GAGCACTCACTCCGAGCTTGGCTGGAGCTATCTGAACCTACTGGGCCCCCTTTCAAC 299
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 Db 245 GAGCATCAACTCCGAGCTTACCTGGAGCTTACCTGAACCTACTGGGCCCCCTTTCAAC 304
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 Db 305 GAGCTGACTTCAATCTCTCTGACTGGGGGAGAAACTTGGCCAGGGGCACTGTTGAC 364
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 QY 360 TTGAGAGGTGTGCGAAGCTCATATGACAACTGCGGCTGACCCAGAACTACGAGGCTTAC 419
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 Db 365 TTGGAAGTGTGCGAAGCTCATATGACAGGCTGCGGCTGACCCAGAACTATGAGGCGTAC 424
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 QY 420 AGCCACTTCTGTGTACTTGTGCTGCTCAACCGTCAAGGCTGCACTGTGAGCTGCGC 479
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 QY 480 CGGAGCTGCGCCCACTTGTGACACGAGCTCCAGGGGCTGTGGGGAGATTTGGGGCGTC 539
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 Db 485 CTTAGCTGTGCGCCCACTTGTGACAGCTTCCAGGGGCTGTGGGGAGATTTGGGGCGTC 544
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 540 ATGAGAGCTGTGGGCTACCACTGCCCGGCTGTGGGAGCTGAACCCACTTGTGACT 599
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 545 ATGGCAGAGCTTGGCTACCACTGCCCGGCTGTGGGAGCTGAACCCACTTGTGACT 604
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 QY 600 CTTGGCCTTGGCCCACTGATGACTTCTTCCAGAAATGACAGACTTGTGCTGAAGAG 659
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 Db 605 CTTGGCCTTGGCCCACTGATGACTTCTTCCAGAAATGATGATGACTTGTGCTGAAGAG 664
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 QY 660 CTGCAAGCTGTGCTGTGGGCGCTCGGCAAGACTTCAACCGGCTCAAGAAAGATGCG 719
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 Db 665 CTGCAAGCTGTGCTGTGGGCGCTCGGCAAGACTTCAACCGGCTCAAGAAAGATGCG 724
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 QY 720 CTTCCAGAGCTGTGCACTGCACTGTGAGGCTCAATGAGCTTGTGACTTGTGACTT 778
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 Db 725 CTTCCAGAGCTGTGCACTGCACTGTGAGGCTCAATGAGGCAATGAGCTTGTGACTTGTGACTT 783
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 RESULT 15
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 XX ABA09140;
 AC
 XX 11-JAN-2002 (first entry)
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 XX Human cardiostrophin-like cytokine homologue cDNA, SEQ ID NO:916.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; actvlin;
 KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; aschna; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial tacheamia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiaesthetic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; vitricide; antibacterial;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 06:10:21 ; Search time 274.709 Seconds
(without alignments)
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Title: US-09-931-704-1
Perfect score: 797
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	19	AAV47510
2	797	100.0	797	19	AAV22652
3	797	100.0	797	21	AAV39481
4	797	100.0	797	24	ABK11647
5	793.4	99.5	881	22	AAH74484
6	793.4	99.5	1790	21	AAH88546
7	759.2	95.3	768	22	AAH9772
8	749.4	94.0	1710	20	AAH16161

Prod. No.	Score	Query Match	Length	DB ID	Description
9	710	89.1	729	22	AAV4201
10	694.8	87.2	1008	22	AAK51548
11	669.4	84.0	819	19	AAV47512
12	669.4	84.0	819	19	AAV22654
13	669.4	84.0	819	21	AAV39483
14	669.4	84.0	819	24	ABK11649
15	668.4	83.9	968	22	AAV09140
16	668.4	83.9	968	22	AAK52532
17	558.4	70.1	648	21	AAH8547
18	523.4	65.7	5087	21	AAV39482
19	523.4	65.7	5087	24	ABK11648
20	523.4	65.7	5088	19	AAV47511
21	523.4	65.7	5088	19	AAV22653
22	493.4	61.9	495	22	ABK11773
23	493.4	61.9	495	22	ABK17855
24	493.4	61.9	495	22	AAK20142
25	493.4	61.9	495	22	AAK46202
26	493.4	61.9	495	22	AAI25564
27	493.4	61.9	495	22	AAI52108
28	493.4	61.9	495	23	ABK45921
29	493.4	61.9	495	24	ABK20512
30	369	46.3	492	22	ABK5256
31	369	46.3	492	22	ABK27996
32	369	46.3	492	22	ABK07469
33	369	46.3	492	22	AAK3253
34	369	46.3	492	22	AAI16384
35	369	46.3	492	22	AAI38047
36	369	46.3	492	23	ABK33003
37	369	46.3	492	24	ABK08085
38	269.4	33.8	283	22	AAH21145
39	80.2	10.1	396	20	ABK16162
40	73.6	9.2	1260	24	ABK16902
41	73.6	9.2	1260	24	ABK16903
42	58.6	7.4	65	24	ABK56698
43	49	6.1	627	20	AAH60797
44	46.8	5.9	1260	24	ABK16904
45	46.8	5.9	1260	24	ABK16905

ALIGNMENTS

RESULT 1
ID AAV47510 standard; cDNA, 797 BP.
XX AAV47510;
AC
XX
DT 09-NOV-1998 (first entry)
XX
XX Human neurotrophic factor NNT-1 cDNA.
DE
XX
XX NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW peripheral neuropathy; dystrophy; neural retina degeneration;
KW common variable immunodeficiency; CVID; selective IgA deficiency;
KW hypogammaglobulinemia; X-linked agammaglobulinemia; antihepatic;
KW therapy; se.
OS
XX Homo sapiens.
XX
XX
XX Key
FH CDS
FT sig_peptide
FT mat_peptide
FT
XX
XX W09833922-A1.
XX
PD 06-AUG-1998.

Human cardiocytrophil
Human polynucleotid
Mouse neurotrophic
cDNA encoding murt
Murine NNT-1 cDNA.
Mouse cDNA encodin
Human cardiocytroph
Human polynucleotid
Mouse interleukin-
Human NNT-1 DNA.
Human novel neurot
Human neurotrophic
Human genomic DNA
Human foetal liver
Probe #16321 for g
Human brain expres
Human bone marrow
Probe #15497 for g
Probe #20794 used
Human liver single
Human genome-deriv
Human foetal liver
Probe #6462 for ge
Human brain expres
Human bone marrow
Probe #6317 for ge
Probe #7733 used t
Human liver single
Human genome-deriv
Osteoarthritis tis
Human cardiocytroph
Oligonucleotide fo
Mouse spliced tran
Human DNAX interle
Oligonucleotide fo
Oligonucleotide fo

XX 02-FEB-1998; 98WO-US02363.
 PF
 XX
 PR 30-JAN-1998; 98US-0016534.
 PR 03-FEB-1997; 97US-0792019.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 PI Chang M, Elliot GS, Sarmiento U, Senaldi G;
 XX
 DR WPI: 1998-437475/37.
 DR P-PSDB; AAM29715.
 XX
 PT Newly isolated nucleic acid encoding human or murine neurotrophic
 PT factor NNT-1 - useful for treatment of neurological and
 PT immunological diseases or inflammation, also as vaccine adjuvant
 XX
 PS Claim 3, Fig 1; 120p; English.

CC This newly isolated human cDNA sequence (deposited at ATCC 98295)
 CC codes for a novel neurotrophic factor, designated NNT-1 (see
 CC AAM29715), that is a growth factor for neurons and for B or T cells.
 CC It was obtained from a T-cell lymphoma cDNA library by expressed
 CC sequence tag analysis on the basis of homology to CNTF. The
 CC isolated NNT-1 cDNA was used as probe to isolate NNT-1 genomic
 CC DNA (see AAV47511). Vectors containing the cDNA or genomic DNA and
 CC host cells are provided for use in the production of NNT-1
 CC polypeptides. These are used to treat: (i) neurological or
 CC immunological diseases, specifically Alzheimer's, Parkinson's or
 CC Huntington's diseases, amyotrophic lateral sclerosis,
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
 CC degeneration of the neural retina, or conditions characterised by T
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),
 CC selective IgA deficiency, hypogammaglobulinemia and X-linked
 CC agammaglobulinemia (claimed), but many others disclosed; and (ii)
 CC inflammation. NNT-1 is also able to boost immunoreactivity and
 CC antibody production following vaccination, and, since it inhibits
 CC tumour necrosis factor production, it may also be useful for
 CC treating sepsis. NNT-1 nucleic acid fragments are also used as
 CC hybridisation probes in diagnostic assays. In addition, cells that
 CC have been engineered to express NNT-1 can be implanted, or nucleic
 CC acids are delivered in gene therapy vectors.

XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;

XX Query Match 100.0%; Score 797; DB 19; Length 797;

XX Best Local Similarity 100.0%; Pred. No. 9.5e-177;

XX Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 CCGCACTCCG 120
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 DB 181 CAGGGGACCCAGGGGCTGGCCCTCCATCAGAAAACCTATACCTCAACCGCTACCTGG 240
 OY 241 AGCACAACCTCGCAGCTTGAGTGGAGCTTATCTGAATCACTTGAGCCCTTTCAAG 300
 DB 241 AGCACAACCTCGCAGCTTGAGTGGAGCTTATCTGAATCACTTGAGCCCTTTCAAG 300
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OY 361 TGAAGTGTGGGAGAACTCAATGACAAATGCTGGGCTGACCCAGAACTACGAGGCTCA 420
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 DB 721 CTCCAGCAGCTGACATCACTTGCACCTGCGGGGCTCATAGCTTGTGACTTGAACCTTCT 780
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 DB 781 CCTCTGGCTCCCGCC 797

RESULT 2

AAV22652
 ID AAV22652 standard; cDNA; 797 BP.

AAV22652;

13-JUL-1998 (first entry)

cDNA encoding human neurotrophic factor NNT-1.

Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
 treatment; neurological disease; degeneration; Parkinson's disease;
 amyotrophic lateral sclerosis; ALS; Alzheimers's disease; stroke; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 90..767

FT /*tag= a

FT sig_peptide 90..170

FT /*tag= b

FT mat_peptide 171..764

FT /*tag= c

US5741772-A.

21-APR-1998.

03-FEB-1997; 97US-0792019.

03-FEB-1997; 97US-0792019.

(AMGE-) AMGEN INC.

Chang M;

WPI: 1998-260526/23.

P-PSDB; AAM56141.

Neurotrophic factor NNT-1 polypeptide and related nucleic acids -

PT useful for stimulating growth of motor and sympathetic neurons
 XX
 PS Dieclojure; Fig 1; 41pp; English.

CC The present sequence encodes a human neurotrophic factor, designated
 CC NNT-1, which is capable of stimulating growth of motor or sympathetic
 CC neurons. The NNT-1 protein is useful in the treatment of neurological
 CC diseases characterized by the degeneration and death of particular
 CC classes of neurons. These diseases specifically include Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC stroke and various degenerative disorders affecting vision.

XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;

Query Match 100.0%; Score 797; DB 19; Length 797;

Best Local Similarity 100.0%; Pred. No. 9.5e-177;

Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATTAAGCTTCCGCGAGCGCGGCTCGCCCTCCCACTCCGCGAGCTCCGGAGAGAG 60
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DB 61 CCGCACCCGCGCGCGCCAGCGCCAGCCCATGAGACCTCCAGACAGGAGACTGCGGAG 120
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DB 721 CTCGAGAGCTGAGTCACTGACCTGAGAGCTGAGGAGCTTCACTTTCGACTTTCGACTTCT 780
OY 781 CCTTCTGCTCCCGCC 797
DB 781 CCTTCTGCTCCCGCC 797

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RESULT 3

AAA39481

ID AAA39481 standard; cDNA; 797 BP.

AC AAA39481;

DT 24-AUG-2000 (first entry)

XX Human NNT-1 cDNA.

XX NNT-1; human; neurotrophic factor; neurotrophic; neuroprotective; treatment;
 KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
 KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 KW Huntington's disease; peripheral neuropathy; neural retina degeneration;
 KW retinopathy; immune disorder; hematopoietic disorder; ss.

OS Homo sapiens.

FN Key Location/Qualifiers

FT CDS 90..767

FT /tag= a

FT /product= "NNT-1"

PN US6054294-A.

PD 25-APR-2000.

PF 12-DEC-1997; 97US-0988819.

PR 03-FEB-1997; 97US-0792019.

XX (AMGE-) AMGEN INC.

PA Chang M;

DR WPI; 2000-338492/29.

DR P-PSDB; AA187813.

PT New nucleic acids encoding neurotrophic factors useful for stimulating
 PT growth of motor or sympathetic neurons for treating neuron cell damage

PS Claim 1a; Fig 1; 42pp; English.

XX This invention describes a novel nucleic acid molecule (I) encoding a
 CC novel neurotrophic factor (NNT-1) (II) which has neurotrophic,
 CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
 CC ophthalmological activity. (I) is useful for producing NNT-1
 CC polypeptides which are useful for treating patients in whom various
 CC cells of the central, autonomic, or peripheral nervous system have
 CC degenerated and/or have been damaged by congenital disease, trauma,
 CC mechanical damage, surgery, stroke, ischemia, infection, metabolic
 CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
 CC proteins are used to treat diseases like Alzheimer's, Parkinson's,
 CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
 CC disease, peripheral neuropathy induced by diabetes or other metabolic
 CC disorders, and/or dystrophies or degeneration of the neural retina such
 CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
 CC night blindness, progressive cone-rod degeneration, immune disorders and
 CC hematopoietic disorders. (I) is effective in treating neurological
 CC conditions and promotes neuron regeneration. Neural functions are
 CC effectively restored in patients suffering from various neurological
 CC disorders. This sequence encodes the human NNT-1 protein described in the
 CC method of the invention.

XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;

Query Match 100.0%; Score 797; DB 21; Length 797;

Best Local Similarity 100.0%; Pred. No. 9.5e-177;

Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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DB 61 CCGGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
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DB 241 AGCAGCACTCCGCGAGCTTGGCGGAGCTATCTGAATCACTGGCGCGCG 300
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DB 541 TGGGAGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
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DB 661 TGGCAACCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
OY 721 CTCGAGAGCTGAGTCACTGCGGCGGCGGCGGCGGCGGCGGCGG 780
DB 721 CTCGAGAGCTGAGTCACTGCGGCGGCGGCGGCGGCGGCGGCGG 780
OY 781 CCTCTTGGCTCCCGCGG 797
DB 781 CCTCTTGGCTCCCGCGG 797

```

```

KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 90..767
FT /tag= a
FT /product= "NNT1"
PN WO200215977-A2.
PD 28-FEB-2002.
PP 17-AUG-2001; 2001WO-US25906.
PR 18-AUG-2000; 2000US-226436P.
PR 16-AUG-2001; 2001US-0931704.
XX (AMGE-) AMGEN INC.
PA Senaldi G;
PI WPI; 2002-280867/32.
DR P-PsDB; AAU78176.
PT Treating Immunoglobulin E-related disease, modulating IGF levels in a
PT patient, preventing IGF-related disease and treating allergic diseases,
PT involves administering NNT-1 inhibitor to a patient
PS Claim 2; Fig 1; 63pp; English.
XX
XX The invention relates to treating Immunoglobulin E (IGE)-related disease,
XX modulating IGF levels in a patient, preventing an IGF-related disease,
XX and treating allergic diseases, comprising administering a
XX therapeutically effective amount of novel neurotrophic factor (NNT)-1
XX inhibitor to a patient. Also included are a method of diagnosing an
XX IGF-related disease or susceptibility to an IGF-related disease, by
XX determining the presence or amount of expression of an NNT1 polypeptide
XX encoded by a NNT1 nucleotide sequence, its fragment or naturally
XX occurring variant, and diagnosing an IGF-related disease or
XX susceptibility of an IGF-related disease based on the presence or amount
XX of expression of the polypeptide and a pharmaceutical composition for use
XX in treating IGF-related disease, comprising the NNT1 inhibitor.
XX The NNT1 inhibitor is useful for preventing and treating IGF-related
XX disease, modulating IGF levels, and treating allergic diseases e.g.
XX Type I allergic disease, allergic rhinitis, eczema, dermatitis,
XX pollinosis, asthma, immune diseases and disorders, diseases involving
XX abnormal cell proliferation including cancer, arteriosclerosis and
XX vascular restenosis, diseases and conditions relating to dysfunction of
XX immune system including rheumatoid arthritis, psoriatic arthritis,
XX inflammatory arthritis, osteoarthritis, inflammatory joint disease,
XX autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
XX bowel disease, transplant rejection, and graft versus host disease, and
XX reproductive diseases and disorders including infertility, miscarriage,
XX preterm labour and delivery, and endometriosis. The present sequence
XX encodes human NNT1.
SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;
Query Match 100.0%; Score 797; DB 24; Length 797;
Best Local Similarity 100.0%; Pred. No. 9.5e-177;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 541 TGGCAGCTTGGGCTTACCACTGCGCCAGCGGCTGCTGGGAGCTGAACTTGGAGCTC 600
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OY 601 CTGGGCTGGCCCACTGAGTGACTTCTCCAGAAATGAGAGCACTTCTGGCTGCTGAAAGAGC 660
DB 601 CTGGGCTGGCCCACTGAGTGACTTCTCCAGAAATGAGAGCACTTCTGGCTGCTGAAAGAGC 660
OY 661 TGCAGACCTGCTGTGCGCTGCGCCAGAGGACTTCAACCGGCTCAAGAAAGATGACAGC 720
DB 661 TGCAGACCTGCTGTGCGCTGCGCCAGAGGACTTCAACCGGCTCAAGAAAGATGACAGC 720
OY 721 CTTCAGACCTGCTGTGCGCTGCGCCAGAGGACTTCAACCGGCTTCTGACTTCTGACCTTCT 780
DB 721 CTTCAGACCTGCTGTGCGCTGCGCCAGAGGACTTCAACCGGCTTCTGACTTCTGACCTTCT 780
OY 781 CCTCTTGGCTCCCCCCC 797
DB 781 CCTCTTGGCTCCCCCCC 797

```

RESULT 5

AAH74484 standard; DNA; 881 BP.

15-OCT-2001 (first entry)

Nucleotide sequence of a human NNT-1 protein.

NNT-1; CLF-1; SCNTFralpha; nervous system; neuron; nervous system;
 neuro-muscular function; tumour; immune system; haematopoietic system;
 amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;
 muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
 blastocyst implantation; thrombosis; retinal disease;
 retinal pigmentosis; ss.

Homo sapiens.

Key Location/Qualifiers
 CDS 174..851
 FT /tag= a
 FT /product= "NNT-1"

```

XX XX WO20015172-A2.
XX XX
XX XX 02-AUG-2001.
XX XX
XX XX 26-JAN-2001; 2001WO-FR00253.
XX XX
XX XX 27-JAN-2000; 2000FR-0001035.
XX XX 12-OCT-2000; 2000FR-0013089.
XX XX
XX XX (FABR ) FABRE MEDICAMENT SA PIERRE.
XX XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX XX
XX XX Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;
XX XX WPI; 2001-488773/53.
XX XX P-PSDB; AAG63543.
XX XX
XX XX A complex comprising a NNT-1 protein and a CLF-1 and/or SCNTFralpha
XX XX protein useful to treat neurodegenerative disease including Parkinson's
XX XX and Huntington's, obesity and cancer
XX XX
XX XX Disclosure; Page 57-58; 67pp; French.
XX XX
XX XX The present sequence encodes a human NNT-1 protein. The specification
XX XX describes a complex comprising a NNT-1 protein and a CLF-1 and/or
XX XX SCNTFralpha protein. The NNT-1/CLF-1 complex is used to modulate
XX XX activity of the SCNTFralpha/gp130/LiFrbeta receptor complex, or to
XX XX induce phosphorylation of the tyrosine of gp130 and LiFrbeta,
XX XX particularly where cells expressing the receptor complex are in the
XX XX central or peripheral nervous system, in neurons implicated in
XX XX neuro-muscular function or in skeletal muscle. The complex or
XX XX antibodies are also used to decrease the survival, growth or
XX XX proliferation of tumour cells or to facilitate the proliferation and/or
XX XX inhibit differentiation of cells stocks. The complex is also used to
XX XX modulate activity of the gp130/LiFrbeta receptor or cells expressing
XX XX CC that receptor, particularly those cells implicated in the immune,
XX XX CC haematopoietic, nervous or reproductive system, the liver or skeletal
XX XX CC muscle. Molecules of the invention may be used to prevent or treat
XX XX CC neurodegenerative diseases including amyotrophic lateral sclerosis,
XX XX CC Parkinson's and Huntington's disease, to repair or regenerate nervous
XX XX CC or muscular tissue or to maintain muscular mass in paralysis patients.
XX XX CC They may also be used to treat cancer, obesity and associated diseases,
XX XX CC and to improve fertility, particularly to avoid endometriosis and/or
XX XX CC assist blastocyst implantation, thrombosis, or retinal disease,
XX XX CC particular retinal pigmentosis.
XX XX
XX XX Sequence 881 BP; 158 A; 318 C; 246 G; 159 T; 0 other;

```

Query Match 99.5%; Score 793.4; DB 22; Length 881;

Best Local Similarity 99.9%; Pred. No. 6.8e-176; Indels 0; Gaps 0;

Matches 794; Conservative 0; Mismatches 1;

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OY 1 ATTAAGCTTGGCCGAGCCGCGGCTGCTCCCACTCCGCGAGCTCCGAGAGAGAG 60
DB 85 ATTAAGCTTGGCCGAGCCGCGGCTGCTCCCACTCCGCGAGCTCCGAGAGAGAG 144
OY 61 CCGACCCGCGGCGCCAGCCGCGGCTGCTCCCACTCCGCGAGCTCCGAGAGAGAG 120
DB 145 CCGACCCGCGGCGCCAGCCGCGGCTGCTCCCACTCCGCGAGCTCCGAGAGAGAG 204
OY 121 TGTAGCGTCTGTGACAGGTGCTCTGACACCTCCCTGACAGTGTGACCTTCAATCGCA 180
DB 205 TGTAGCGTCTGTGACAGGTGCTCTGACACCTCCCTGACAGTGTGACCTTCAATCGCA 264
OY 181 CAGGGGACCCAGGGGCTGGGCTCCCTCATCAGAAAACTATGACTTACCCGCTTACCTG 240
DB 265 CAGGGGACCCAGGGGCTGGGCTCCCTCATCAGAAAACTATGACTTACCCGCTTACCTG 324
OY 241 AGCACCACTCCGACGCTTGGTGGGACCTATCTGAACCTGAGGCCCCCTTTCACAG 300
DB 325 AGCACCACTCCGACGCTTGGTGGGACCTATCTGAACCTGAGGCCCCCTTTCACAG 384

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QY 301 AGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCAGAGGCGCACTGTGACT 360
DB 385 AGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCAGAGGCGCACTGTGACT 444
QY 361 TGGAGGTGGGGAAGCTTCATGAGAACTGGGGTGCACCAAGAACTGAGAGGCTTACA 420
DB 445 TGGAGGTGGGGAAGCTTCATGAGAACTGGGGTGCACCAAGAACTGAGAGGCTTACA 504
QY 421 GCCACCTTGTGTTACTTGGCGGCTCAACCGTCAAGGCTGCACTGCTGAGCTGGCGC 480
DB 505 GCCACCTTGTGTTACTTGGCGGCTCAACCGTCAAGGCTGCACTGCTGAGCTGGCGC 564
QY 481 GCAGCTGGGCGCACTTCTGACACAGCTTCAGAGGCGCTGCTGGGAGCACTTGGGCGTCA 540
DB 565 GCAGCTGGGCGCACTTCTGACACAGCTTCAGAGGCGCTGCTGGGAGCACTTGGGCGTCA 624
QY 541 TGGGAGCTTGGGCTTACCACTGCGCCAGCGCTGCTGGGAGTGAACCACTTGGAGCTC 600
DB 625 TGGGAGCTTGGGCTTACCACTGCGCCAGCGCTGCTGGGAGTGAACCACTTGGAGCTC 684
QY 601 CTGGGCGCTGGCGCACTGCTCTGCAAGAGTGAAGCACTTGGGCTGCTGAAGGAGC 660
DB 685 CTGGGCGCTGGCGCACTGCTCTGCAAGAGTGAAGCACTTGGGCTGCTGAAGGAGC 744
QY 661 TGCAGACCTGGCTGGCGCTGGCGCCAGGACTTCAACCGGCTCAAGAGAGAGATGCGAGC 720
DB 745 TGCAGACCTGGCTGGCGCTGGCGCCAGGACTTCAACCGGCTCAAGAGAGAGATGCGAGC 804
QY 721 CTGCAGAGCTGAGTCACTGACCTGCGACCTGGGGGCTGATGCTTGACTTGAACCTTCT 780
DB 805 CTGCAGAGCTGAGTCACTGACCTGCGACCTGGGGGCTGATGCTTGACTTGAACCTTCT 864
QY 781 CCTTTCGCTGCCCC 795
DB 865 CCTTTCGCTGCCCC 879

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RESULT 6

AAA88546
ID AAA88546 standard; DNA; 1790 BP.

AAA88546;

22-JAN-2001 (first entry)

Human interleukin-B60 (IL-B60) gene.

Interleukin-B60; IL-B60; human; cytokine; chromosome 11;

cytokine-like factor-1; haematopoietic; inflammation;

antiflammatory; autoimmune disease; therapy; ds.

Homo sapiens.

Key Location/Qualifiers

FT CDS 162..809

FT sig_peptide 162..212

FT mat_peptide 213..806

FT tag= b

FT tag= c

FT tag= c

FT tag= c

FT tag= c

FT tag= c

DR WPI; 2000-587426/55.

DR P-PSDB; AAB19686.

PT Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,

PT polypeptides, and nucleic acids, useful in research, diagnosis and for

PT treating inflammatory and autoimmune disorders -

PS Claim 17; Page 15-16; 97pp; English.

The present sequence is that of DNA encoding human interleukin-B60 (IL-B60, see AAB19586), a novel, small soluble cytokine-like protein of 198 amino acids that exhibits structural motifs characteristic of a member of the long-chain cytokines, and which shows homology to granulocyte colony stimulating factor and interleukin-6. IL-60B may have either stimulatory or inhibitory effects on haematopoietic cells, including e.g. lymphoid cells, such as T-cells, B-cells, natural killer cells, macrophages, dendritic cells, haematopoietic progenitors, etc. Methods are provided for modulating the physiology or development of a cell or tissue culture cells by contacting the cell with an agonist or antagonist of IL-B60 or an agonist of antagonist of a complex of mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see AAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological factor in motor neuron development and regeneration. IL-60B, its agonists and antagonists may be used to treat inflammatory or autoimmune disorders and also for drug screening. The IL60B gene maps to human chromosome 11.

SQ Sequence 1790 BP; 381 A; 560 C; 474 G; 375 T; 0 other:

Query Match 99.5%; Score 793.4; DB 21; Length 1790;

Best Local Similarity 99.9%; Pred. No. 7.9e-176;

Matches 794; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATTAAGCTTGGCGGAGCCGCGGCTGCGCTCCCACTCCGCGAGCTCCGAGAGAG 60
DB 43 ATTAAGCTTGGCGGAGCCGCGGCTGCGCTCCCACTCCGCGAGCTCCGAGAGAG 102
QY 61 CCGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 103 CCGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 162
QY 121 TGTAGCGTGCCTGTCAGCGTGTGCTTGGGACCTCCCTGCGAGTGCAGCTTCAATCGCA 180
DB 163 TGTAGCGTGCCTGTCAGCGTGTGCTTGGGACCTCCCTGCGAGTGCAGCTTCAATCGCA 222
QY 181 CAGGGAGCCAGGGGCTGGGCTGCTTCATCCAGAAAACCTATGACTCACCCTGACTGG 240
DB 223 CAGGGAGCCAGGGGCTGGGCTGCTTCATCCAGAAAACCTATGACTCACCCTGACTGG 282
QY 241 AGCACCAATCGGAGCTGGGCTGGGACCTATGAACTACTGGGCGCCCTTCAACG 300
DB 283 AGCACCAATCGGAGCTGGGCTGGGACCTATGAACTACTGGGCGCCCTTCAACG 342
QY 301 AGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCAGAGGCGCACTGTGACT 360
DB 343 AGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCAGAGGCGCACTGTGACT 402
QY 361 TGGAGGTGGGGAAGCTTCATGAGAACTGGGGTGCACCAAGAACTGAGAGGCTTACA 420
DB 403 TGGAGGTGGGGAAGCTTCATGAGAACTGGGGTGCACCAAGAACTGAGAGGCTTACA 462
QY 421 GCCACCTTGTGTTACTTGGCGGCTCAACCGTCAAGGCTGCACTGCTGAGCTGGCGC 480
DB 463 GCCACCTTGTGTTACTTGGCGGCTCAACCGTCAAGGCTGCACTGCTGAGCTGGCGC 522
QY 481 GCAGCTGGGCGCACTTCTGACACAGCTTCAGAGGCGCTGCTGGGAGCACTTGGGCGTCA 540
DB 523 GCAGCTGGGCGCACTTCTGACACAGCTTCAGAGGCGCTGCTGGGAGCACTTGGGCGTCA 582
QY 541 TGGGAGCTTGGGCTTACCACTGCGCCAGCGCTGCTGGGAGTGAACCACTTGGAGCTC 600
DB 583 TGGGAGCTTGGGCTTACCACTGCGCCAGCGCTGCTGGGAGTGAACCACTTGGAGCTC 642

```

QY 601 CTGGCCCTGCCAGTGAATTCTCTCAGAGATGAGACGACTTCTGGCTGTGAAGAGAC 660
DB 643 CTGGCCCTGCCAGTGAATTCTCTCAGAGATGAGACGACTTCTGGCTGTGAAGAGAC 702
QY 661 TGCAGACCTGGCTGTGGCGCTCGCGCCAGAGACTTCAACCGGCTCAAGAGAGATGACAC 720
DB 703 TGCAGACCTGGCTGTGGCGCTCGCGCCAGAGACTTCAACCGGCTCAAGAGAGATGACAC 762
QY 721 CTGCAGACCTGAGTCACTGACCTGTGGGCTCATATGGCTTCTGACCTTCTTCT 780
DB 763 CTGCAGACCTGAGTCACTGACCTGTGGGCTCATATGGCTTCTGACCTTCTTCT 822
QY 781 CCTCTCGCTCCCGCC 795
DB 823 CCTCTCGCTCCCGCC 837

RESULT 7
AAH99772
ID AAH99772 standard; cDNA, 768 BP.
XX AAH99772;
XX
XX 16-OCT-2001 (first entry)
DE Human protein encoding cDNA sequence SEQ ID NO:607.
XX
XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
XX anti-inflammation; anti-rheumatic; anti-arthritic; immunosuppressive;
XX anti-bacterial; endocrine; cardiac; central nervous system; virucide;
XX anti-HIV; fungicide; antimutagen; cardiovascular; anti-nausea; anaemia;
XX antiaggregant; haemostatic; vulnery; antitumor; osteopathic; eczema;
XX dermatological; anti-allergic; antiscabetic; antidiabetic; cytostatic;
XX neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
XX immunosuppressive; gene therapy; anti-asthma therapy; vaccine; inflammation;
XX anti-infective; rheumatoid arthritis; septic shock; pancreatitis;
XX cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
XX genetic disease; haematopoietic disorder; platelet disorder; asthma;
XX chromocytoma; osteoporosis; severe combined immunodeficiency;
XX allergic rhinitis; diabetes; multiple sclerosis; depression;
XX Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
XX neurological disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200153455-A2.
XX
XX 26-JUL-2001.
XX
XX 22-DEC-2000; 2000MO-US55017.
XX
XX 23-DEC-1999; 99US-0471275.
XX 21-JAN-2000; 2000US-048725.
XX 25-APR-2000; 2000US-0552317.
XX
XX (HYSE-) HYSE INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457603/49.
XX P-PSDB; AAM25831.
XX
XX Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
XX Claim 1; Page 638; 1217pp; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
XX CC AAM25963. The proteins can have activities based on the tissues and
XX CC cells they are expressed in, such as: anti-inflammatory; anti-rheumatic;
XX CC anti-arthritic; immunosuppressive; antibacterial; endocrine; cardiac;
XX CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;

CC cardiovascular; anti-nausea; antiaggregant; haemostatic; vulnery;
CC anti-ulcer; osteopathic; dermatological; anti-allergic; anti-asthma;
CC anti-diabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, chromocytoma, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.

SQ Sequence 768 BP; 137 A; 278 C; 217 G; 136 T; 0 other;
XX
XX

Query Match 95.3%; Score 759.2; DB 22; Length 768;
Best Local Similarity 99.6%; Pred. No. 6,4e-168;
Matches 761; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATTAAGCTTGGCCGAGCCGCGGCTCGCCTCCACTCCGCGACCTCCGAGAGAGAG 60
DB 5 ATTAAGCTTGGCCGAGCCGCGGCTCGCCTCCACTCCGCGACCTCCGAGAGAGAG 64
QY 61 CCGCACCCGCGCGCGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAG 120
DB 65 CCGCACCCG 124
QY 121 TGTTCGCGGCTGTGACGCGGCTGTGACCTCTGACCTCTGACCTCTGACCTCTGAC 180
DB 125 TGTTCGCGGCTGTGACGCGGCTGTGACCTCTGACCTCTGACCTCTGACCTCTGAC 184
QY 181 CAGGCGACCCGAGGCGCTGCGCCCTCCATCCAGAAACCTATGACTCAACCGCTACCTG 240
DB 185 CAGGCGACCCGAGGCGCTGCGCCCTCCATCCAGAAACCTATGACTCAACCGCTACCTG 244
QY 241 AGCACCACTCCGCGAGCTTGGCTGGGACCTATCTGACCTCTGACCTCTGACCTCTGAC 300
DB 245 AGCACCACTCCGCGAGCTTGGCTGGGACCTATCTGACCTCTGACCTCTGACCTCTGAC 304
QY 301 AGCGAGCTTCAACCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 305 AGCGAGCTTCAACCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 364
QY 361 TGGAGGTGTGGGAGGCTCAATGACAACTGCGGCTGACCCGAGACTTACGAGGCTTACA 420
DB 365 TGGAGGTGTGGGAGGCTCAATGACAACTGCGGCTGACCCGAGACTTACGAGGCTTACA 424
QY 421 GCGACCTTGTGTGTAATGCTGGCTGACCGTCAACCGTCAAGCTGCTGAGCTGCGCG 480
DB 425 GCGACCTTGTGTGTAATGCTGGCTGACCGTCAACCGTCAAGCTGCTGAGCTGCGCG 484
QY 481 GCGACCTGCGCACTTGTGACCACTGCAAGGCTGCGGCTGCGGAGCACTTGGGCGCTCA 540
DB 485 GCGACCTGCGCACTTGTGACCACTGCAAGGCTGCGGCTGCGGAGCACTTGGGCGCTCA 544
QY 541 TGGCAGCTTGTGGCTTACCACTGCGCGCGCGCTGCGGAGCTTACCACTTGGAGCTG 600
DB 545 TGGCAGCTTGTGGCTTACCACTGCGCGCGCGCTGCGGAGCTTACCACTTGGAGCTG 604
QY 601 CTGGCCCTGCCAGTGAATTCTCTCAGAGATGAGACGACTTCTGGCTGTGAAGAGAC 660
DB 605 CTGGCCCTGCCAGTGAATTCTCTCAGAGATGAGACGACTTCTGGCTGTGAAGAGAC 664
QY 661 TGCAGACCTGGCTGTGGCGCTCGCGCCAGAGACTTCAACCGGCTCAAGAGAGATGACAC 720
DB 665 TGCAGACCTGGCTGTGGCGCTCGCGCCAGAGACTTCAACCGGCTCAAGAGAGATGACAC 724
QY 721 CTGCAGACCTGAGTCACTGACCTGTGGGCTCATATGGCTTCTGACCTTCTTCT 764

PT /cag= C
PT /product= "Human mature cardiotrophin-like cytokine
PT (CLC) protein"
XX
XX
PN W0200127157-A1.
XX
XX
PD 19-APR-2001.
XX
XX
PF 06-OCT-2000; 2000WO-AV01216.
XX
XX
PR 08-OCT-1999; 99AU-0003327.
XX
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PR 12-MAY-2000; 2000AU-0007489.
XX
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX
PI Nash A, Jachno KM, Pabri LJ, Reid K, Bartlett PR, Hilton DJ;
PI Nakata Y, Haegawa M;
XX
XX
DR MPI; 2001-281978/29.
XX
XX
DR P-PSDB; AAE00828.
XX
XX
PT New biologically active complex comprising NR6 and
PT cardiotrophin-like cytokine, for facilitating proliferation,
PT differentiation and/or survival of a cell -
XX
XX
PS Claim 31; Page 112-114; 123pp; English.
XX
XX
CC The present invention relates to a biologically active complex comprising
CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC).
CC The complex is useful in the manufacture of a medicament for the
CC treatment and/or prophylaxis of a subject, as it is involved in
CC facilitating proliferation, differentiation and/or survival of a cell.
CC The complex or its components have neurotrophic activity. The present
CC sequence is human cardiotrophin-like cytokine (CLC) cDNA.
XX
XX
SQ Sequence 729 BP; 132 A; 261 C; 196 G; 140 T; 0 other;
XX
XX
Query Match 89.1%; Score 710; DB 22; Length 729;
Best Local Similarity 100.0%; Pred. No. 2e-156;
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
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QY 86 CCCCATGAGACTTCGAGAGAGGAGCTCGTGGGGAGATTAGCGCTGTGACGGTGTCT 145
DB 7 CCCCATGAGACTTCGAGAGAGGAGCTCGTGGGGAGATTAGCGCTGTGACGGTGTCT 66
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XX
QY 146 CTGGCACTCTCCCTGCGAGTGCAGCTCTCAATGCGACAGGGGAGCCAGGGGCTTGGCCCTTC 205
DB 67 CTGGCACTCTCCCTGCGAGTGCAGCTCTCAATGCGACAGGGGAGCCAGGGGCTTGGCCCTTC 126
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QY 206 CATCGAAGAAACCTATGACCTCAACCGGCTACCTGAGGACCAATCCGAGAGCTTGGCTGG 265
DB 127 CATCGAAGAAACCTATGACCTCAACCGGCTACCTGAGGACCAATCCGAGAGCTTGGCTGG 186
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XX
QY 266 GACCTATCTGAACTACTCTGGGCCCCCTTTCAACGAGCCAGACTTCACTCCCGCT 325
DB 187 GACCTATCTGAACTACTCTGGGCCCCCTTTCAACGAGCCAGACTTCACTCCCGCT 246
XX
XX
QY 326 GGGGGGAGAGACTCTGCGGAGGAGGAGCTGTTGACTTGAAGGTGTGGCGAAAGCTTCATGA 385
DB 247 GGGGGGAGAGACTCTGCGGAGGAGGAGCTGTTGACTTGAAGGTGTGGCGAAAGCTTCATGA 306
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QY 386 CAAACTGGGGCTGACCCAGAGACTAGAGGCTTACAGCCACTTCTGTGTTACTTGGCTGG 445
DB 307 CAAACTGGGGCTGACCCAGAGACTAGAGGCTTACAGCCACTTCTGTGTTACTTGGCTGG 366
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QY 446 CCTCAACCTGACAGCTGCTGCTGAGCTGCGCCGAGCTTGGCCACTTCTGACACAG 505
DB 367 CCTCAACCTGACAGCTGCTGCTGAGCTGCGCCGAGCTTGGCCACTTCTGACACAG 426
XX
XX
QY 506 CCTTCAGGGGCTTGGGAGAGCTTGGGGGCTGATGAGGAGCTTCTGGGCTACCCACTGCC 565
DB 427 CCTTCAGGGGCTTGGGAGAGCTTGGGGGCTGATGAGGAGCTTCTGGGCTACCCACTGCC 486

QY 566 CCAGCCGCTGCTGGGAGCTGAACCCACTTGAATCTCTGGGCCCTGCGCCACAGTGAATTCCT 625
DB 487 CCAGCCGCTGCTGGGAGCTGAACCCACTTGAATCTCTGGGCCCTGCGCCACAGTGAATTCCT 546
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XX
QY 626 CCAGAGATGAGACGACTTCTGCTGCTGAGAGGAGCTGACAGCTTGGCTGTGGCTCGGC 685
DB 547 CCAGAGATGAGACGACTTCTGCTGCTGAGAGGAGCTGACAGCTTGGCTGTGGCTCGGC 606
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QY 686 CAAGACTTCAACCGGCTCAAGAGAGATGACAGCTGACAGCTGACAGCTGACCTTCA 745
DB 607 CAAGACTTCAACCGGCTCAAGAGAGATGACAGCTGACAGCTGACAGCTGACCTTCA 666
XX
XX
QY 746 CTGGGGGCTGATGAGCTTCTGACTTGAACCTTCTCTTCTGCTGCTGCTGCTGCTGCT 795
DB 667 CTGGGGGCTGATGAGCTTCTGACTTCTGACTTCTCTTCTGCTGCTGCTGCTGCTGCT 716
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RESULT 10
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ID AAKS1548 standard; cDNA; 1008 BP.
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AC AAKS1548;
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DT 06-NOV-2001 (first entry)
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DE Human polynucleotide SEQ ID NO 93.
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KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
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OS Homo sapiens.
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PN W0200157190-A2.
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PD 09-AUG-2001.
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PF 05-FEB-2001; 2001WO-US04098.
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PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX
PA (HYSE-) HYSEQ INC.
XX
XX
PI Tang YT, Liu C, Dymnac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang Y, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX
DR MPI: 2001-476283/51.
XX
XX
PT P-PSDB; AAM78415.
XX
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
XX
PS Claim 1; Page 711-712; 6221pp; English.
XX
XX
CC The invention relates to polynucleotides (AAKS1456-AAKS3435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and


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source
1..569
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-40-G02"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then deapped with tabacco acid
pyrophosphatase (TAP). The deapped intact mRNA was
ligated with DNA-RNA linker including EcoRI site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."
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BASE COUNT 135 a 192 c 151 g 91 t

ORIGIN

Query Match 57.6%; Score 458.8; DB 12; Length 569;
Best Local Similarity 99.6%; Pred. No. 2.1e-88;
Matches 460; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATTAAGCTTGGCCGGAGCCGGGCTCCGCCCTCCCACTCCGCCAGCTCCGGGAGAGAG 60
DB 108 ATTAAGCTTGGCCGGAGCCGGGCTCCGCCCTCCCACTCCGCCAGCTCCGGGAGAGAG 167
QY 61 CCGCACCCCGCCGGCCAGCCAGCCCATGAGACTCCGAGCAGGGGACTGTGGGGGA 120
DB 168 CCGCACCCCGCCGGCCAGCCAGCCCATGAGACTCCGAGCAGGGGACTGTGGGGGA 227
QY 121 TGTAGCGTCTGTGACGAGTGTCTTGACCTTCCCTGACGTGCCAGCTCAATCGCA 180
DB 228 TGTAGCGTCTGTGACGAGTGTCTTGACCTTCCCTGACGTGCCAGCTCAATCGCA 287
QY 181 CAGGGGACCCAGGGGCTGGCCCTCCATCCAGAAAACCTGACCCGCTACCTGG 240
DB 288 CAGGGGACCCAGGGGCTGGCCCTCCATCCAGAAAACCTGACCTGACCTGACCTGA 347
QY 241 AGCACCAACTCCGACGCTTGGGACTATCTGAACCTAGGAGCCCTTTCAAG 300
DB 348 AGCACCAACTCCGACGCTTGGGACTATCTGAACCTAGGAGCCCTTTCAAG 407
QY 301 AGCCAGACTTCAACCTTCCCGCTGGGGGAGAGACTTGCCAGGGCCACTGTGACT 360
DB 408 AGCCAGACTTCAACCTTCCCGCTGGGGGAGAGACTTGCCAGGGCCACTGTGACT 467
QY 361 TGGAGGTGGGGAAGCCCTCAATGACAACTGGGCTGACCCAGAACTACGAGGCTACA 420
DB 468 TGGAGGTGGGGAAGCCCTCAATGACAACTGGGCTGACCCAGAACTACGAGGCTACA 527
QY 421 GCCACCTTCTGTGTACTTGTGAGCTCAACGCTCAGGCTG 462
DB 528 GCCACCTTCTGTGTACTTGTGAGCTCAACGCTCAGGCTG 569

Search completed: February 9, 2004, 09:23:57
Job time : 2160.8 secs

QY 309 TTCAACCCCTCCCGCCTGGGGGAGAGACTCTGCCAGGGGCACTGTGACTTGGAGGTG 368
 DB 238 TTCAACCCCTCCCGCCTGGGGGAGAGACTCTGCCAGGGGCACTGTGACTTGGAGGTG 357
 QY 369 TGGCGAAGCTCAATGACAACTGCGGCTGAGCCAGAACTAGAGGCTTACAGCCACTT 428
 DB 358 TGGCGAAGCTCAATGACAACTGCGGCTGAGCCAGAACTAGAGGCTTACAGCCACTT 417
 QY 429 CTGTGTACTTGGTGGGCTCAACGCTGAGGCTGAGCTGAGCTGGCGGAGCCCTG 488
 DB 418 CTGTGTACTTGGTGGGCTCAACGCTGAGGCTGAGCTGAGCTGGCGGAGCCCTG 477
 QY 489 GCCCACTTGTGACCAAGCCTTCCAGGGGCTGTGGGAGGATTTGCGGAGCTTACAGGAGCT 548
 DB 478 GCCCACTTGTGACCAAGCCTTCCAGGGGCTGTGGGAGGATTTGCGGAGCTTACAGGAGCT 537
 QY 549 CTGGG 553
 DB 538 CTGGG 542

RESULT 14
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 LOCUS K-EST0127535 S13KMS5 Homo sapiens cDNA clone S13KMS5-57-A03 5',
 DEFINITION mRNA sequence.
 ACCESSION BM847924 GI:19204323
 VERSION BM847924.1 GI:19204323
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 529)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished
 TITLE JOURNAL
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 57 row: A column: 03
 High quality sequence stop: 529.
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 /organism="Homo sapiens"
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 /lab_host="Top10F"
 /clone_lib="S13KMS5"
 /note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI. The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then deapped with tobacco acid
 pyrophosphatase (TAP). The deapped intact mRNA was
 ligated with DNA-RNA linker including EcoR I site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dt-selected mRNA by priming with
 dt-tailed vector. The dt-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10F by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA

BASE COUNT 92 a 199 c 147 g 91 t
 ORIGIN
 Query Match 64.6%; Score 514.8; DB 12; Length 529;
 Best Local Similarity 99.4%; Pred. No. 2e-100;
 Matches 527; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 31 CTCGCCACTCCGACCTCCCGGAGAGAGAGCCGACCCGCGGAGCCGAGCCCA 90
 DB 1 CTCGCCACTCCGACCTCCCGGAGAGAGAGCCGACCCGCGGAGCCGAGCCCA 60
 QY 91 TGAACCTCCGAGACAGAGGAATCTGTGGAGATTTAGTCGTGTGACAGTGTCTGGC 150
 DB 61 TGAACCTCCGAGCA-GGAGCTGTGGGGGATTTAGTCGTGTGACAGTGTCTGGC 119
 QY 151 ACCTCCCTGACAGTGCACAGCTCTCAATGCAACAGGGGACCCAGGGCTTGGCCCTCATCC 210
 DB 120 ACCTCCCTGACAGTGCACAGCTCTCAATGCAACAGGGGACCCAGGGCTTGGCCCTCATCC 179
 QY 211 AGAAACCTATGACCTCACCCGCTACCTGGAGACCAACTCCGAGCTTGGCTGGGACCT 270
 DB 180 AGAAACCTATGACCTCACCCGCTACCTGGAGACCAACTCCGAGCTTGGCTGGGACCT 239
 QY 271 ATCTGAATCACTGTGGGCCCCCTTTCAACGAGCAGACTTCAACCTCCGCTGGGGG 330
 DB 240 ATCTGAATCACTGTGGGCCCCCTTTCAACGAGCAGACTTCAACCTCCGCTGGGGG 299
 QY 331 CAGAGACTCTGCGCCAGGGGCACTGTGTAAGTGGAGGTGTGGAGAGCTCAATGACAAAC 390
 DB 300 CAGAGACTCTGCGCCAGGGGCACTGTGTAAGTGGAGGTGTGGAGAGCTCAATGACAAAC 359
 QY 391 TGGCGCTACCCAGAACTACAGAGGCTACAGACACTTCTGTGTACTTGTGGCTGTCA 450
 DB 360 TGGCGCTACCCAGAACTACAGAGGCTACAGACACTTCTGTGTACTTGTGGCTGTCA 419
 QY 451 ACCGTCAAGCTGCGCAGCTGCTGAGTGCAGCCGAGGCTGAGCCCACTTGTGACAGCTTCC 510
 DB 420 ACCGTCAAGCTGCGCAGCTGCTGAGTGCAGCCGAGGCTGAGCCCACTTGTGACAGCTTCC 479
 QY 511 AGGGCTGCTGCGGAGCAATTTGGGGGCTGATGAGCTTGTGGGCTTACCCA 560
 DB 480 AGGGCTGCTGCGGAGCAATTTGGGGGCTGATGAGCTTGTGGGCTTACCCA 529

RESULT 15
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 DEFINITION mRNA sequence.
 ACCESSION BM846748 GI:19203147
 VERSION BM846748.1 GI:19203147
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 569)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished
 TITLE JOURNAL
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 40 row: G column: 02
 High quality sequence stop: 569.
 Location/Qualifiers

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 /note="Vector: pcns; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 90 a 195 c 148 g 89 t
 ORIGIN

Query Match 65.3%; Score 520.4; DB 12; Length 522;
 Best Local Similarity 99.8%; Pred. No. 1.3e-101;
 Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

31 CTCCTCACTCCGACGCTCCGAGAGAGAGCCGCGCCGCGCCAGCCGCGCA 90
 1 CTCCTCACTCCGACGCTCCGAGAGAGAGCCGCGCCGCGCCAGCCGCGCA 60
 91 TGGACCTCCGACGAGGAGCTGCTGGGGGATGTTAGCGCTGTCAGAGGCTCTGGC 150
 61 TGGACCTCCGACGAGGAGCTGCTGGGGGATGTTAGCGCTGTCAGAGGCTCTGGC 120
 151 ACCTCCCTGACAGTGCAGCTCTCAATCGACAGGGAGCCAGGAGCTGCGCCCTCATCC 210
 121 ACCTCCCTGACAGTGCAGCTCTCAATCGACAGGGAGCCAGGAGCTGCGCCCTCATCC 180
 211 AGAAAACTATGACTACCCGCTACCTGGAGACCACTCCGACGCTTGGTGGAGCT 270
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 271 ATCTGAACACTGGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGCCCTGGGG 330
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 331 CAGAGACTCTGGCCAGGAGCACTGTGACTTGAAGGTGGGAGAGCTCATGACAAAC 390
 301 CAGAGACTCTGGCCAGGAGCACTGTGACTTGAAGGTGGGAGAGCTCATGACAAAC 360
 391 TGGGCTGACCCAGAACTACAGAGGCTTACAGCCACCTTGTGTATCTTGCCTGAC 450
 361 TGGGCTGACCCAGAACTACAGAGGCTTACAGCCACCTTGTGTATCTTGCCTGAC 420
 451 ACCGTCAGGCTGCTGCTGAGCTGGCGGAGAGCTGGCCACTTTCGACACCACTTC 510
 421 ACCGTCAGGCTGCTGCTGAGCTGGCGGAGAGCTGGCCACTTTCGACACCACTTC 480
 511 AGGGCTGCTGGGAGCACTTGGGGGCTCATGGAGAGCTTGG 552
 481 AGGGCTGCTGGGAGCACTTGGGGGCTCATGGAGAGCTTGG 522

RESULT 13
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 DEFINITION K-EST0089713 S19N665307 Homo sapiens cDNA clone S19N665307-9-G05
 ACCESSION BM821005

VERSION BM821005.1 GI:19177418
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 542)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 9 row: G column: 05
 High quality sequence stop: 542.
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 location/Qualifiers
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 /note="Organ: Stomach; Vector: pcns; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 92 a 202 c 155 g 92 t 1 others
 ORIGIN

Query Match 65.0%; Score 518.4; DB 12; Length 542;
 Best Local Similarity 98.2%; Pred. No. 3.4e-101;
 Matches 535; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

9 TTCGCGGAGCGCGGCTCGCCCTCCACTCCGCCAGCTTCGAGAGAGAGCCGACCC 68
 1 TTCGCGGAGCGCGGCTCGCCCTCCACTCCGCCAGCTTCGAGAGAGAGCCGACCC 57
 69 GCGCGGCCAGCCCGAGCCCATGAGACTCGAGAGAGGAGCTGCTGGGGATGTTACG 128
 58 GCGCGGCCAGCCCGAGCCCATGAGACTCGAGAGAGGAGCTGCTGGGGATGTTACG 117
 129 TGCCTGTCAGAGTGTCTGACACTCCCTGACAGTGCAGACTCTCATTCGACAGAGGAG 188
 118 TGCCTGTCAGAGTGTCTGACACTCCCTGACAGTGCAGACTCTCATTCGACAGAGGAG 177
 189 CGAGGCTCTGCGCCCTCCATCCAGAAACTATGACTTCACCCGCTACCTGGAGACCA 248
 178 CGAGGCTCTGCGCCCTCCATCCAGAAACTATGACTTCACCCGCTACCTGGAGACCA 237
 249 CTCGCGACCTTGGCTGGAGACTATCTGAACCTACCTGGGCGCCCTTTCAAGAGGACAC 308
 238 CTCGCGACCTTGGCTGGAGACTATCTGAACCTACCTGGGCGCCCTTTCAAGAGGACAC 297

Db	566	ACTTGTGCTGCTGAAGAGGCTGCACCTTGGCTGTGGCGCTCGGCCCAAGGACTTCAAC	625
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LOCUS	BM846370		
DEFINITION	BM846370	532 bp	mRNA
ACCESSION	K-EST0125376	SL1KMS5s1	Homo sapiens cDNA clone SL1KMS5s1-21-A09 5'
VERSION	BM846370		mRNA sequence.
KEYWORDS	BM846370.1	GI:19202769	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 532)		
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.W., Park,H.S., Kim,S. and Kim,Y.S.		
	21C Frontier Korean EST Project 2001		
	Unpublished		
TITLE	Contact: Kim YS		
JOURNAL	Genome Research Center		
COMMENT	Korea Research Institute of Bioscience & Biotechnology		
	52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea		
	Tel: +82-42-860-4470		
	Fax: +82-42-860-4409		
	Email: yongsung@mail.kribb.re.kr		
	Plate: 21 row: A column: 09		
	High quality sequence stop: 532.		

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FEATURES
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location/Qualifiers
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/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10p"
/clone_idb="S13KMS5s1"
/notes="Vector: pcns; Site 1: EcoRI; Site 2: NotI; The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decayed with tobacco acid
pyrophosphatase (TAP). The decayed intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10p' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library. After analyzing and sequencing about 2,000 ~
3,000 colonies in original cDNA library, the abundant
cDNAs were selected and amplified by PCR reaction using
vector region primer including T7 promoter as 5' primer
and N(NT)14 as 3' primer. The PCR products were used as
template for synthesis of biotinylated single stranded cDNA
by in vitro transcription reaction. The synthesized RNA
probes were hybridized with antisense single stranded
cDNAs prepared from original library and incubated with
avidin-gel. After removing DNA-RNA hybrids by centrifuge,
the subtracted cDNA libraries were constructed by
transformation of the remaining DNA into competent cells E.
coli Top10p' with electroporation method."

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ORIGIN

Query Match	66.3%;	Score 528.8;	DB 12;	Length 532;
Best Local Similarity	99.6%;	Pred. No. 2e-103;		
Matches 530;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

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QY	91	TGACCTTCGACGACAGGGGACTCTGTGGGGGATGTTAGCTGCTGTGCAGGTGCTTGCG	150
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QY	151	ACCTCCCTGCGAGTGCAGCTCTCAATGCGACAGAGGGAGCCAGAGGCGTGGACCCCTCATCC	210
Db	121	ACCTCCCTGCGAGTGCAGCTCTCAATGCGACAGAGGGAGCCAGAGGCGTGGACCCCTCATCC	180
QY	211	AGAAACCTATGACTGACCTGACCCGCTAAGCTGAGACCAACTCCGACGTTGGCTGGGACCT	270
Db	181	AGAAACCTATGACTGACCTGACCCGCTAAGCTGAGACCAACTCCGACGTTGGCTGGGACCT	240
QY	271	ATCTGAACCTACCTGGGGCCCCCTTTTCAACGAGCGACAGATTCAACCTCCCGGCTGGGGG	330
Db	241	ATCTGAACCTACCTGGGGCCCCCTTTTCAACGAGCGACAGATTCAACCTCCCGGCTGGGGG	300
QY	331	CAGAGACTTGCGCCAGGGGCACTGTGTGACTTGAAGGTGTGGCGAAGCTCTATGACAAC	390
Db	301	CAGAGACTTGCGCCAGGGGCACTGTGTGACTTGAAGGTGTGGCGAAGCTCTATGACAAC	360
QY	391	TGCGGCGTACCCGAACTACGAGGGCTTACAGCCACTTCTGTGTACTTGGGTGGGCTTCA	450
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QY	451	ACCGTCAAGGCTGCACATGCTGAGGCTGGCGCAGACTTGGGCCACTTTCGACCAAGCTCC	510
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QY	511	AGGGCTGCTGTGGGAGACATTCGGGGGCTCAATGGCAAGCTTGGGGCTACCCACT	562
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[illegible]

BASE COUNT 190 a 339 c 283 g 212 t 4 others
 ORIGIN

Query Match 71.7%; Score 571.2; DB 9; Length 1028;
 Best Local Similarity 97.5%; Pred. No. 1.9e-112;
 Matches 591; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

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 250 TCCGAGCTGGAGCTGGAGCTATCTGAATCACTGGAGCCCTCTTCAACAGCCAGACT 309
 105 TCCGAGCTGGAGCTGGAGCTATCTGAATCACTGGAGCCCTCTTCAACAGCCAGACT 164
 310 TCAACCTTCCTCCGCTGGGAGGAGAGACTCTGCCCAGAGCCACTGTGAATTGAGGTGT 369
 165 TCAACCTTCCTCCGCTGGGAGGAGAGACTCTGCCCAGAGCCACTGTGTGAGGTGT 224
 370 GCGGAAGCTCAATGACAACTGCGGCTGACCCAGAACTACAGAGCCCTACAGCCCTTC 429
 225 GCGGA--CTCAATGACAACTGCGGCTGACCCAGAACTACAGAGCCCTACAGCCCTTC 282
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 730 CTGAGTACCTCTGAGCACTGGGGGCTGATGGCTTCTGACTTCTGACTTCTCTCTGGC 789
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 790 TCCCC 795
 643 TCCCC 648

RESULT 10
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 ID HSM090574
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 XX BX497225.1
 SV BX497225.1
 XX 09-MAY-2003 (Rel. 75, Created)
 DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp779H1332_r1 (from clone DKFZp779H1332)
 XX
 XX EST; expressed sequence tag.
 XX
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 XX
 RN (1)

RP 1-634
 RA Othenwelder B., Obermaier B., Deutchenhaur S., Mewes H.W., Weill B.,
 RA Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
 RL MIPs, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
 XX
 CC This is the 5' sequence of the clone insert
 CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 CC sequenced by MedGenomix (Martinried/Germany) within the cDNA
 CC No. 51 sequence consortium of the German Genome Project.
 CC This clone (DKFZp779H1332) is available at the RZPD in Berlin.
 CC Please contact the RZPD: Ressourcenzentrum Neuherberg 6,
 CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX
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 FT /tissue="liver"
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Query Match 69.0%; Score 549.8; DB 2; Length 634;
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 Matches 591; Conservative 0; Mismatches 14; Indels 4; Gaps 3;

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QY	660	CTGCAGACCTG	670
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RESULT 8
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BM840863				
DEFINITION	K-EST0118015 S13KMS5 Homo sapiens CDNA clone S13KMS5-35-D11 5',			

mRNA sequence.

VERSION BM840863.1 GI:19197272

SOURCE Homo sapiens (human)

REFERENCE

QUALITY OF

TITLE

JOURNAL
COMMENT

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52, Eoeun-dong, Yuseong-gu, Daejeon 305-333, South Korea
Tel.: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribb.re.kr
Plate: 35 row: D column: 11
High quality sequence stop: 573.
Location/Qualifiers
1. 573

FEATURES	Location/Qualifiers
source	1. .573

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="S13KMS5-35-D11"
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/clone_id="S13KMS5"
/notes="vector: pcnss; Site_1: EcoRI; Site_2: NotI; The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoR I which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

```

Query Match	71.7%	Score	571.4	' DB	12	Length	573
Best Local Similarity	99.8%	Pred.	No. 1.5e-112				
Matches	572	Conservative	1	Indels	0	Gaps	0

Qy	Qy	Db	Qy
3.1	CTCCACCTCCGCGCAGACCTTCGCGGAGAGAGACCGACACCGGGCGGGCCCACTCCCGAGCCCA	90	
1	CTCCACCTCCGCGCAGACCTTCGCGGAGAGAGACCGACACCGGGCGGGCCCACTCCCGAGCCCA	60	
9.1	TGAGACTTCGAGACAGAGGAGACTTCGTGGGGGATGTTAGCGTCTGTGACAGGTGCTCTGGC	150	
6.1	TGAGACTTCGAGACAGAGGAGACTTCGTGGGGGATGTTAGCGTCTGTGACAGGTGCTCTGGC	120	

QY	15	ACCTCCCTGACGGGACGCTCTCATGCAACAGGGGACCCAGGGGCTGGGCCCTCATCC	210
Db	121	ACCTCCCTGACGGGACGCTCTCAATGCAAGGGGACCCAGGGGCTGGGCCCTCATCC	180
QY	211	AGAAAACTATGACCTCACCCGCTACCTGGAGCACACTCCGAGCTTGGCTGGGACT	270
Db	181	AGAAAACTATGACCTCACCCGCTACCTGGAGCACACTCCGAGCTTGGCTGGGACT	240
QY	271	ATTGGAACCTAGGGGCCCCCTTTCAACAGAGCCAGACTTAAACCTCCCGCTGGGGG	330
Db	241	ATTGGAACCTAGGGGCCCCCTTTCAACAGAGCCAGACTTAAACCTCCCGCTGGGGG	300
QY	331	CAGAGACTGTGCCAGGGGCACTGTGACTTGGAGGTGGCGAAGCTCAATGACAAAC	390
Db	301	CAGAGACTGTGCCAGGGGCACTGTGACTTGGAGGTGGCGAAGCTCAATGACAAAC	360
QY	391	TGCGGCTGACCCAGAACTACAGAGGCTTACAGCCACTTTGTGTTACTTGGTGAGCTCA	450
Db	361	TGCGGCTGACCCAGAACTACAGAGGCTTACAGCCACTTTGTGTTACTTGGTGAGCTCA	420
QY	451	ACCGTACAGGCTGCACCTGTGAGCTGGGCGGACGCTGGGCCACTTGTGACACAGGCTCC	510
Db	421	ACCGTACAGGCTGCACCTGTGAGCTGGGCGGACGCTGGGCCACTTGTGACACAGGCTCC	480
QY	511	AGGGGCTGTGGGACAGACTTGGGGGCTCATGGAGCTTGGGCTACCACTGGCCAGC	570
Db	481	AGGGGCTGTGGGACAGACTTGGGGGCTCATGGAGCTTGGGCTACCACTGGCCAGC	540
QY	571	CGTGCTGTGGAGTGAACCACTTGGACTTCTTG 603	
Db	541	CGTGCTGTGGAGTGAACCACTTGGACTTCTTG 573	

Db 541 CGCTGCCCTGGACTGAACCCACTTGACTCCTG 573

RESULT 9	AL543945	1028 bp	linear	EST 31-MAY-200
LOCUS	AL543945			
DEFINITION	Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS001D04YM15 5-PRIME, mRNA sequence.			

ACCESSION	AL543945
VERSION	AL543945.2
	GI:31265790

SOURCE Homo sapiens (human)

444

REFERENCE

COLLECTION
TITLE

COMMENT

CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, **Web :** www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6127.r For
 more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI004AG080P1&cluster=6127.r)
[cgi-bin/cluster.cgi?seq=CSODI004AG080P1&cluster=6127.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI004AG080P1&cluster=6127.r). **Contact :**
 Peng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODI004AG080P1.
FEATURES
 source
 Location/Qualifiers
 1..1028

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/clone-1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V

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 |||||
 DB 542 CGCTGCTGGAGTGAACCCACTTGACTCTGCGCCCTG 580
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RESULT 7
 BY735168
 LOCUS BY735168
 DEFINITION BY735168 RIKEN full-length enriched, mammary gland RCB-0527 Jy9-MC(B) cDNA Mus musculus cDNA clone G930015G22 5', mRNA sequence.

ACCESSION BY735168
 VERSION BY735168
 KEYWORDS BY735168.1 GI:27148295
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)

REFERENCE AUTHORS
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Balderelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chochia, C., Corbani, L. E., Cousin, S., Dalia, E., Dragani, T. A., Fletcher, C. P., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustlich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedierski, R. M., Kling, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wymshaw-Bois, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carinini, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, K., Asakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterson, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
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 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Watanabe, M. and Hayashizaki, Y. Direct Subcloning
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multipillar sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

location/Qualifiers

1. 678
 /organism="Mus musculus"
 /mol_type="mRNA"
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 BASE COUNT 124 a 237 c 190 g 126 t 1 others
 ORIGIN

Query Match 72.3% Score 576.4; DB 14; Length 678;
 Best Local Similarity 92.1%; Pred. No. 1,3e-113;

Matches 618; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

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 DB 8 ATTAAAGCTTGGCCGAGACCCGAGCTGACCTCCACCTCCGAGCTCCGAGAGAGAG 67
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 QY 61 CCGACCCGCGCGCCAG-CCCAAGCCCATGACCTCCGAGAGGAGGACTCTGGGGG 119
 DB 68 CCGGCG 127
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 QY 120 ATGTGAGTGGCTGTGAGAGGTGTCTGTGAGACCTCCCTGAGAGGCGGACTCTAATGC 179
 DB 128 ATGTGAGTGGCTGTGAGAGGTGTCTGTGAGACCTCCCTGAGAGGCGGACTCTAATGC 187
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 QY 180 ACAGGAGGACCCAGGAGGCTCGGCGCTCCATCCAGAAACCTATGACCTACCGGCTACCTG 239
 DB 188 ACAGGAGTCCAGGAGGCTCGGCGCTCCATCCAGAAACCTATGACCTACCGGCTACCTG 247
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 QY 240 GAGCACCACCTCGCAGCTTGGTGGACCTATGTAACCTAGGCGCCCTTTCAAC 299
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 QY 300 GAGCCACCTTCAACCTTCCCGCTGGGGGCAAGACTTGGCCAGGCGCACTGTGAC 359
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 QY 360 TTGAGAGTGGCGGAGGCTCAATGACCAATGCGGGCTGACCCAGAACTAGAGGCTTAC 419
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 DB 428 AGTACACCTCTGTGTATTCTTCTGAGCTTCAACGCTGAGGCTGACCTGAGCTGAGCTGGC 487
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 DB 488 CCGACCTGCGCCACTTGTGACCAAGCTTCAAGGCTGCTGGGCAAGCATTTGGGGCTC 547
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 QY 540 ATGGAGCTTGGGCTACCACTGAGCCGAGCGGCTGAGGCTGAGGCTGAGGCTGAGGCT 599
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KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1053)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

CDNA library preparation: Life Technologies, Inc.
DNA library arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LML10246 row: m column: 14
High quality sequence start: 3
High quality sequence stop: 675.

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Oy	80	CCCCAG-CCCCATGACCTTCGAGCAGGGAGCTCGTGGGGGATTTTAACTGTGCTGTGA	138
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Dp	122	CGGTGCTTGGCACCTTCCTGCAGTGCCAGCTTCMAATGCAACAGGGGACCCAGGGCTTG	181
Oy	199	GCCCTTCATTCAGAAACCTATGACCTTCAACCCGCACTGGAGCACAATTCGCGAGCT	258
Dp	182	GCCCTTCATTCAGAAACCTATGACCTTCAACCCGCACTGGAGCACAATTCGCGAGCT	241
Oy	259	TGCGTGGAGCTTACTGAACCTACTTGGGGCCCCC---TTTCACGAGCCAGACTTCAAC	314
Dp	242	TGCGTGGAGCTTACTGAACCTACTTGGGGCCCCCGTTTCAACTAGCGCTTGAATTCAC	301
Oy	315	CTCTCCCGGCTGGGGGACAGACTCG-CCGAGGGCCACTGTGACTTGGAGGTGTGGCG	373
Dp	302	CTCTCCCGGCTGGGGGACAGACTCTGTCCCAAGGGCACTGTTGACTTGGAGGTGTGGCG	361
Oy	374	AAGCTTCATGACAAACTGCGGCTGACCCAGAACTACGAGGCTTACAAGCCTTCTGTG	433
Dp	362	AAGCTTCATGACAAACTGCGGCTGACCCAGAACTACGAGGCTTACAAGCCTTCTGTG	421
Oy	434	TTAATTGCGTGGCTCAACCTTGAAGGCTGCATCTGTAGAGTGTGCCCGCACTTGGCCA	493
Dp	422	TTAATTGCGTGGCTCAACCTTGAAGGCTGCATCTGTAGAGTGTGCCCGCACTTGGCCA	481

Qy	493	CTTCTGCACAGCTCTCAGGGGCTCTGCTGGAGAGATTGGGGGGCTCATGAGAGCTCTGGG	553
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Db	602	CACAGTGAATCTCTCTCAGAGAGATGAGACGACTTCTGGCTGTGAGAGAGAGCTGCACACTGG	661
Qy	672	CTGTGGCGCTCGGCGCAAGGACTTCAACCGGCTCAAGAGAAGATGCAGGCTCTCGACGCT	721
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Qy	732	GCAGTACACCTGCACCTGGGGGGCTCATGGCTTCTGACTTCTGACACTT	778
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RESULT 5	
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LOCUS	
DEFINITION	BW763333 594 bp mRNA linear EST 04-MAR-2002
ACCESSION	K-EST0044645 S13KMS5 Homo sapiens cDNA clone S13KMS5-18-E09 5' ,
VERSION	BW763333 mRNA sequence.
KEYWORDS	BW763333 .1 GI:19092948
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 594)
Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.

TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished
COMMENT	Contact: Kim YS

FEATURES

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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 18 row E column: 09
High quality sequence stop: 594.
Location/Qualifiers

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SOURCE
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/notes="Vector: pcns; Site_1: EcoRI; Site_2: NotI; The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10f by electroporation method. The cDNA libraries

```


Db	238	GGGCCCCCCTTTCAACGAGCCAGAATTCAAACCTTCCCCTCGGAGGAGACTTCCTGC	297
Oy	334	CAGGGCCACTGTGACTTGAGAGTGTGGCGAAAGCTCATATGACAATACTGCCGTGAACCCA	403
Db	298	CAGGGCCACTGTGACTTGAGAGTGTGGCGAAAGCTCATATGACAATACTGCCGTGAACCCA	357
Oy	404	GAACTACAGAGGCTACAGCCACTCTCTGTGTTACTTGTGTGGAGCCCAACCGTAAGGCTGC	463
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Oy	464	CAGTGTAGCTGCGCCGCGAGCTTGGCCCACTTTCGACACAGACCCTCCAGGGCTGTCTGG	523
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Db	538	TGAACCCACTTGGACTCTCTGGGCGCTGGCCCAAGTACATTTCTCCAGAAAGATGAGACATT	597
Oy	644	CTGGCTGCTGAGAGGAGCTGCAGACCTGTGCTGGGCGTGGCGAAGACCTTCAACCGGCT	703
Db	598	CTGGCTGCTGAGAGGAGCTGCAGACCTGTGCTGGGCGTGGCGAAGACCTTCAACCGGCT	657
Oy	704	CAGAAGAAGATGACAGCCTCCAGCAGCTGCAGTCAACCTCGACCTGGAGG--CTCATGGC	761
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Oy	762	TTCTGACTTTCGACCTTCTCTCTTGTGCTTCCCCC 797	
Db	718	TTCTGACTTTCGACCTTCTCTCTTGTGCTTCCCCC 753	
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ACCESSION	BG437538		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 853)		
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgabs@email.nih.gov Tissue Procurement: DCTD/DTP/Gasdar cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.liml.gov Plate: L1CM1384 row: 1 column: 19 High quality sequence stop: 761. Location/Qualifiers 1..853		

Query Match	80.5%	Score 641.6	DB 10	Length 853
Best Local Similarity	96.9%	Pred. No. 1.4e-127		
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BASE COUNT 154 a 301 c 232 g 166 t
 ORIGIN

into EcoRI/XhoI sites using the following 5' adaptor:
 GGCCAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC Library."

QY	52	GGAGAAGAGCCGCAACCCGCGCCGACCCCAAGCCCACTGAGCTCCGACAGAGGACT	111
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QY	112	CGTGGGGGATTTTATGCGTCTGTGCAAGGTCTCTGAGCACTCCCTTGACATGCGAGCTC	171
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QY	232	GCTACCTTGAGACCAACTCCGCAAGCTTGGCTGGGACCTATCTGAATTACTTGGGCCCCC	291
DB	181	GCTACCTTGAGACCAACTCCGCAAGCTTGGCTGGGACCTATCTGAATTACTTGGGCCCCC	240
QY	292	CTTTCAAGSAGCCAGACTTCAACCCCTCCCGCTGGGGGGAGAGACTCTGCGCCAGGGCCA	351
DB	241	CTTTCAAGSAGCCAGACTTCAACCCCTCCCGCTGGGGGGAGAGACTCTGCGCCAGGGCCA	300
QY	352	CTGTGATCTTGAAGGTGTGGGAAAGCTCAATGACAACTGCGGCTGACCCAGAACTAG	411
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QY	472	AGCTGGCGCGAGGCTGGCCCACTTTGCAACAGCCTCCAGGGGCTGTGGGGAGCACTTG	531
DB	421	AGCTGGCGCGCA - CTTGGCCCACTTTGCAACAGCCTTCCAGGGGCTGTGGGGAGCACTTG	479
QY	532	CGGCGCTCATGGGCACTCTGGGCTTACCAC - TGCCCCAGCGGCTGCTGGGAC - TGAACC	589
DB	480	CGGCGCTCATGGGCACTCTGGGCTTACCAC - TGCCCCAGCGGCTGCTGGGAC - TGAACC	539
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QY	650	GCTGAAGGAGGTGAGACCTGGGCTGGGCGCTGGGCCAAGGACTTCAAA - CGGCTCAAGA	708
DB	600	GCTGAAGGAGGTGAGACCTGGGCTGGGCGCTGGGCCAAGGACTTCAAA - CGGCTCAAGA	659
QY	709	AGAAGATGACAGCTCCAG - CAGCTGACGTCAACC - TGACACTGGGGGCTCATGAGCTTC	764
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 LOCUS 60234555F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4453813 5',
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 ACCESSION BG164929.1 GI:12671563

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/clone_1lb="NIH MGC 101"
/note="Organism: lung; Vector: pORF7; Site_1: EcorI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcorI/XhoI sites using the following 5' adaptor: GGGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene), Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
BASE COUNT 154 a 325 c 240 g 167 t 1 others
ORIGIN

Query Match 92.9%; Score 740.4; DB 13; Length 887;
Best Local Similarity 99.7%; Pred. No. 8.9e-149;
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68 CGGCAACCGGCG 127
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Db 728 CTTGGAGAGCTTGGGAGAGCTCAATGACAAATGCGGCTGAGCTGAGTGAAGAG 761

RESULT 2
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LOCUS AGENCOURT 8864294 Lupski sciatic_nerve Homo sapiens cDNA clone
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ACCESSION BQ940483 GI:22355961
VERSION BQ940483.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1157)
NIH-MGC http://mgs.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13608 row: 9 column: 03
High quality sequence stop: 572.

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source

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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
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Directionally cloned using the following adaptors:
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5'-GACTAGTCTGATCGCAGGCGCGCGCGCTT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
BASE COUNT 221 a 374 c 346 g 216 t
ORIGIN
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164 GCAGCTTCAATGACAGAGGAGCCAGAGGCTGCGCTTCATCCAGAAACTTATGA 223
118 GCAGCTTCAATGACAGAGGAGCCAGAGGCTGCGCTTCATCCAGAAACTTATGA 177
224 CTTACCCGCTACCTGGAGACCAACTCCGAGCTTGGCTGGAGCTATCGAATACCT 283
178 CTTACCCGCTACCTGGAGACCAACTCCGAGCTTGGCTGGAGCTATCGAATACCT 237
284 GGGCGCGCGCTTTCACAGAGCCAGACTTCACCTCCCGCTGGGAGGAGAGACTTGGC 343

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

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(without alignments)
9002.070 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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12: gb_est3:*
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16: em_estom:*
17: em_gss_hum:*
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19: em_gss_pln:*
20: em_gss_vrt:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	656.4	82.4	1157	13	BQ940483
3	641.6	80.5	853	10	BG437538
4	621	77.9	1053	10	BG164929

5	590.8	74.1	594	12	BM763333
6	577.4	72.4	580	12	BM848189
7	576.4	72.3	678	14	BY735168
8	571.2	71.7	1028	12	BM840863
9	571.2	71.7	1028	9	AL543945
10	549.8	69.0	634	2	HS090574
11	528.8	66.3	532	12	BM846370
12	520.4	65.3	522	12	BM841897
13	518.4	65.0	542	12	BM821005
14	514.8	64.6	529	12	BM847924
15	458.8	57.6	569	12	BM846748
16	439.6	55.2	831	29	CC138171
17	412	51.7	476	10	BE632644
18	405.4	50.9	420	12	BM764238
19	403.4	50.6	458	12	BM363136
20	387	48.6	407	9	AT752561
21	379.8	47.7	448	13	BY531444
22	371.4	46.6	482	12	BM846622
23	331.2	41.6	505	4	BX528877
24	329.6	41.4	388	13	BY022718
25	319.8	40.1	668	14	BY734701
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29	258.4	32.4	392	13	BY012378
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35	222	27.9	357	13	BY185798
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ALIGNMENTS

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DEFINITION AGENCOURT 8813192 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6428214
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ACCESSION BQ948158
VERSION BQ948158.1 GI:22363636
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: L1CM2614 row: h column: 07
High quality sequence stop: 674.

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Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	3603	AGGGCTGTGGGCAAGATTGGGGGCTGATGGCACTGTGGGCTACCACTGGCCAGG	3662
QY	571	CGCTGCTGGGACTGAACCACTTGGACTCTGGCCCTGCCCCACAGTGAATTCTCCAGA	630
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QY	631	AGATGACGACTTCTGGCTGTGAGAGAGCTGCAACCTTGTGCGCTGGCCAAAG	690
DB	3723	AGATGACGACTTCTGGCTGTGAGAGAGCTGCAACCTTGTGCGCTGGCCAAAG	3782
QY	691	ACTTCAACCGGCTCAGAGAGAGATGACAGCTTCACAGCTGACACCTTGCACTGG	750
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Job time : 3206.36 secs

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Best Local Similarity 98.2%; Pred. No. 3.3e-111;
Matches 601; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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DB 1366 GAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1425
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RESULT 14
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ACCESSION AR002596
VERSION AR002596.1 GI:3964150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 5087)
AUTHORS Chang, M.-S.
TITLE Neurotrophic factor NRT-1
JOURNAL Patent: US 5741772-A 3 21-APR-1998;
FEATURES
source location/Qualifiers
BASE COUNT 992 A 1746 C 1191 G 1158 T
ORIGIN

Query Match 65.7%; Score 523.4; DB 6; Length 5087;
Best Local Similarity 99.8%; Pred. No. 8.3e-97;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 ATCTGACTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 330
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QY 331 CAGAGACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 390
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DB 3723 AGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3782
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LOCUS Sequence 3 from Patent WO0215977.
DEFINITION
ACCESSION AX392088
VERSION AX392088.1 GI:19700576
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Senaldi, G.
TITLE Methods and compositions for treating ige-related disease using nu

JOURNAL
Patent: WO 0215977-A 3 28-FEB-2002;
Amgen Inc. (US)

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ACCESSION	AF176913
VERSION	AF176913.1
GI	6007644

KEYWORDS	
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE
AUTHORS
1 (bases 1 to 819)
Senaldi, G., Varnum, B.C., Sarmiento, U., Starnes, C., Lile, J.,

Scully, S., Guo, J., Elliott, G., McIninch, J., Shaltee, C. L.,
 Freeman, D., Mann, F., Simonet, W. S., Boone, T. and Chang, M. S.
 Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
 IL-6 family
 JOURNAL
 Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)

MEDLINE 99432294
 PUBMED 10500198
 REFERENCE 2 (bases 1 to 819)
 AUTHORS Senaldi,G., Varum,B., Sarmiento,U., Lile,J., Starnes,C.,
 Scully,S., Guo,J., Elliott,G., McIninch,J., Freeman,D., Shaklee,C.,
 Mann,F., Simoner,S., Boone,T. and Chang,M.-S.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive,
 Thousand Oaks, CA 91320, USA
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QY	61	CCGCAACCCGGCCGGCCGACG-CCCGAGCCCAATGACCTCCGAGCAGGGGACCTCGTGGGG	113
Db	65	CCGCCCCCGGCGCGCCCGGCCCCCGACGCCCAATGACCTCCGAGCAGGGGACCTCGTGGGG	124
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QY	300	GAGCCAGACTTCAACCTCCGCCCTGGGGGGCAGAGACTGCCCCAGGGCCACTGTGAC	359
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QY	420	AGCCACTTCTGTGTACTTTCGTGGTGGCTCAACCGTCAAGGCTGCCACTGTGAGCTGCGC	479
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QY	540	ATGGCAGCTCTGGGCTTACCCCACTGGCCCGAGCCGCTGCGGAGCTGAAGCCCACTTGGACT	599
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QY	720	CCTCCAGAGCTTGAGTCAACCTCAGCACTCGGGGGCTCATGTGCTTGTGACTTGTGACCTT	778
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DEFINITION	Sequence 19 from Patent WO0155219.		Linear
			PAT 30-AUG-2001

ACCESSION	AA205060
VERSION	AX205060.1
KEYWORDS	GI:15394299
SOURCE	synthetic construct
ORGANISM	synthetic construct
OTHER	artificial sequences.

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AUTHORS	Elson, G. and Gauchat, J.F.
TITLE	Secretin/nut-1 fusion protein
JOURNAL	Patent: WO 0155219-A 19 02-AUG-2001;
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ORGANISM Unknown.
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AUTHORS 1 (bases 1 to 819)
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JOURNAL Neutrotrophic factor NNT-1
Patent: US 5741772-A 4 21-APR-1998;
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source 1..819
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Query Match 84.0%; Score 669.4; DB 6; Length 819;
Best Local Similarity 92.0%; Pred. No. 1.8e-126;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTTAAAGCTTGGCCGGAGCCGGGCTCGCCCTCCCACTCCGCGAGGAGAGAG 60
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DEFINITION Sequence 4 from Patent WO0215977.
ACCESSION AX392089
VERSION AX392089.1 GI:19700577
KEYWORDS
SOURCE
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Senaldi, G.
TITLE Methods and compositions for treating ige-related disease using m
JOURNAL t-1 inhibitors
Patent: WO 0215977-A 4 28-FEB-2002;
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Best Local Similarity 92.0%; Pred. No. 1.8e-126;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTTAAAGCTTGGCCGGAGCCGGGCTCGCCCTCCCACTCCGCGAGGAGAGAG 60
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DB 425 AGTCACTCTGTGTGTTACTTGGTGGCTTCAACCGTCAAGGCTGCGCACTGAGCTGCGC 484
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 ACCESSION
 VERSION
 KEYWORDS
 ORGANISM
 SOURCE
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 680)
 Hu.X., Xu.Y., Zhang.B., Peng.X., Yuan.J. and Qiang.B.
 Direct Submission
 Submitted (30-JUL-2001) Department of Biochemistry, Institute of
 Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong
 Dan San Tiao, Beijing 100005, P.R. China
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 VERSION AR002597.1 GI:3964151
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IMAGE:4453813, mRNA, complete cds.
ACCESSION BC012939
VERSION BC012939.1 GI:15277894
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 1736)
Strausberg R.
Direct Submission
Submitted (20-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villaloboscm.tmc.edu.
Villalobos, D.K., Luna, R.A., Hale, S.M., Huliyil, S., Lu, X., Garcia,
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781 CCTCTTGGCTGCGCC 795
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Db 865 CCTCTTGGCTGCGCC 879

RESULT 5
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LOCUS
DEFINITION Sequence 1 from Patent WO0155219.
ACCESSION AX205042
VERSION AX205042.1 GI:15394277
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Elson, G. and Gauchat, J.F.
Scientif/nnt-1 fusion protein
Patent: WO 015219-A 1 02-AUG-2001;
PIERRE FABRE MEDICAMENT (FR)
FEATURES
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CDS

BASE COUNT 158 a 318 c 246 g 159 t
ORIGIN

Query Match 99.5%; Score 793.4; DB 6; Length 881;
Best Local Similarity 99.9%; Pred. No. 9.2e-152;
Matches 794; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY		661	TGCAGACCCTGTGTGGCGCTCGGCCAAGAGATTTCACCGGCTCAAGAAGATGACGC	720
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LOCUS				
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ACCESSION	complete cds.			
VERSION	AF176911			
KEYWORDS	AF176911.1 GI:6007640			
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 797) Senaoli,G., Varnum,B.C., Sarmiento,U., Lille,J., Starnes,C., Scully,S., Guo,J., Elliott,G., McIninch,J., Shalee,C.L., Freeman,D., Manu,F., Simonet,W.S., Boone,T. and Chang,M.-S. Novel neurotrophin-1/B-cell-stimulating factor-3: a cytokine of the TF-beta family			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)			
MEDLINE	99433254			
PUBMED	10500198			
REFERENCE	2 (bases 1 to 797) Senaoli,G., Varnum,B., Sarmiento,U., Lille,J., Starnes,C., Scully,S., Guo,J., Elliott,G., McIninch,J., Freeman,D., Shalee,C., Manu,F., Simonet,W.S., Boone,T. and Chang,M.-S. Direct Submission Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive, Thousand Oaks, CA 91320, USA			
TITLE	Journal			
FEATURES	Source			
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QY	121	TGTTAGCGTGCCTGTGACAGCGTGCTCTTGGAACCTTCCTGCACTGCGAGCTTCAATCGCA	180
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LOCUS			linear
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VERSION	AX205024.1		GI:15394259
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1		
FEATURES	Elson, G., Gauchat, J.F., Plun-Favreau, H., Chevalier, S. and Gascan, H.		
SOURCE	Isolated complex comprising a nnt-1 protein and in addition at		
	least a Clf-1 protein and/or a scntfr_9(a) protein		
	Patent: WO 0155172-A 1 02-AUG-2001;		
	PIERRE FABRE MEDICAMENT (FR) ; INSTITUT NATIONAL DE LA SANTE ET DE		
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	source		

Source 1..797
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BASE COUNT 139 a 297 c 218 g 143 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.7e-152;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX392086
DEFINITION Sequence 1 from Patent WO0215977.
ACCESSION AX392086
VERSION AX392086.1 GI:19700574
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Senaldi, G.
TITLE Method and compositions for treating age-related disease using m
t-1 inhibitors
JOURNAL Patent: WO 0215977-A 1 28-FEB-2002;
Amgen Inc. (US)
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ORIGIN

Query Match 100.0%; Score 797; DB 6; Length 797;
Best Local Similarity 100.0%; Pred. No. 1.7e-152;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 TGGAGGTGTGGGAGGCTCAATGACAACTCGGCTGACCCAGAACTACGAGGCGCTACA 420
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GenCore version 5.1.6
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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	793.4	99.5	881	6	AX205024
5	793.4	99.5	881	6	AX205042
6	776.4	97.4	1736	9	BC012939
7	749.4	94.0	1689	9	AF172854
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ALIGNMENTS

RESULT 1
LOCUS AR002595
DEFINITION Sequence 1 from patent US 5741772.
ACCESSION AR002595
VERSION AR002595.1 GI:3964149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 797)
AUTHORS Chang, M.-S.
TITLE Neurotrophic factor NNT-1
JOURNAL Patent US 5741772-A 1 21-APR-1998;
FEATURES location/contigs